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OM protein - protein search, using sw model

Run on: June 15, 2005, 12:13:24 ; Search time 42 Seconds
(without alignments)
682.506 Million cell updates/sec

Title: US-10-642-289-2

Perfect score: 384

Sequence: 1 MDPAGPRGVLPKPCRLVL.....CVERPPSMKQQMPPEPL 384

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	336	87.5	384	4	US-09-970-516-2
3	320	83.3	368	4	US-10-053-510-21
4	264	68.8	312	4	US-09-949-016-9811
5	250	65.1	384	4	US-09-949-016-7026
6	209	54.4	293	4	US-09-796-487-3
7	107	27.9	204	4	US-09-205-258-328
8	55	14.3	119	4	US-09-796-487-9
9	33	8.6	63	4	US-09-205-258-788
10	33	8.6	63	4	US-09-959-897-13
11	33	8.6	63	4	US-09-959-897-21
12	33	8.6	373	4	US-09-796-487-5
13	33	8.6	381	4	US-09-796-487-1
14	33	8.6	381	4	US-09-796-487-4
15	33	8.6	382	4	US-09-970-516-6
16	33	8.6	388	4	US-09-817-676A-15
17	33	8.6	388	4	US-09-796-487-2
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19	17	4.4	46	4	US-09-959-897-23
20	17	4.4	52	4	US-09-959-897-10
21	17	4.4	52	4	US-09-959-897-18
22	16	4.2	53	4	US-09-959-897-12
23	16	4.2	53	4	US-09-959-897-20
24	15	3.9	47	4	US-09-959-897-14
25	15	3.9	47	4	US-09-959-897-22
26	13	3.4	47	4	US-09-959-897-9
27	13	3.4	54	4	US-09-959-897-17

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30	11	2.9	49	4	US-09-959-897-24	Sequence 24, Appl
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33	8	2.1	225	4	US-09-252-991A-28646	Sequence 28646, A
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44	7	1.8	62	4	US-09-732-210-1585	Sequence 1585, Ap
45	7	1.8	71	3	US-08-858-207A-540	Sequence 540, App
46	7	1.8	83	4	US-09-270-767-61454	Sequence 61454, A
47	7	1.8	87	4	US-09-107-433-4959	Sequence 4959, Ap
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55	7	1.8	256	4	US-09-252-991A-30033	Sequence 30033, A
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63	7	1.8	328	3	US-09-527-657-9	Sequence 9, Appl
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81	7	1.8	700	4	US-09-684-708A-2	Sequence 2, Appl
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154	6	1.6	83	2	US-08-853-021-2	Sequence 2, Appl	227	6	1.6	118	3	US-09-098-789-1	Sequence 1, Appl
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169	6	1.6	94	3	US-08-300-928C-2	Sequence 2, Appl	242	6	1.6	123	4	US-09-462-606-64	Sequence 64, Appl
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395	6	1.6	214	3	US-08-664-855-3	Sequence 3, Appl	468	6	1.6	252	3	US-08-097-869-3	Sequence 3, Appl
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979 6 1.6 538 4 US-09-543-681A-4490 Sequence 4490, Ap
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981 6 1.6 543 4 US-09-107-532A-3717 Sequence 3717, Ap
982 6 1.6 543 4 US-09-438-185A-748 Sequence 748, App
983 6 1.6 545 3 US-08-974-180-15 Sequence 15, Appl
984 6 1.6 545 4 US-09-544-683-2 Sequence 2, Appli
985 6 1.6 545 4 US-10-192-419-2 Sequence 2, Appli
986 6 1.6 546 4 US-09-266-965-134 Sequence 134, App
987 6 1.6 547 4 US-09-252-991A-26732 Sequence 26732, A
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990 6 1.6 549 4 US-09-270-767-45421 Sequence 45421, A
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995 6 1.6 552 4 US-09-071-035-430 Sequence 430, App
996 6 1.6 553 4 US-09-491-356C-24 Sequence 24, Appl
997 6 1.6 553 4 US-09-830-123-17 Sequence 17, Appl
998 6 1.6 553 4 US-09-902-540-14945 Sequence 14945, A
999 6 1.6 555 2 US-08-793-229-34 Sequence 34, Appl
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ALIGNMENTS

RESULT 1
US-09-959-897-2
; Sequence 2, Application US/09959897
; Patent No. 6730480
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/09/959,897
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-897-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 2, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-516-2

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Db 241 LEEPVPSSHWTVPDDEFVLVLALHSHLGSEMFAAPMGRCAGVWHLFYVRAGVSRAMLL 300
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RESULT 3
US-10-053-510-21
; Sequence 21, Application US/10053510
; Patent No. 6830881
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrtst, Henrik

; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-510-21

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DB 301 PYLVVVPVVAFRLEPKDGK 320

RESULT 4
US-09-949-016-9811
; Sequence 9811, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9811
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9811

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QY 193 TLGTFRLAALTYRGLAYLPVGRVSKTTPASPVVQQGPDVAHLVPLEEPVPSHWTVP 252
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DB 241 EYECPLYVVPVVAFRLEPKDGK 264

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; Sequence 7026, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7026
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7026

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US-09-796-487-3
; Sequence 3, Application US/09796487

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; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(384)
; OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, corresponding to the amino acid residue 1 to 384 of Homo sapiens SPHK-1 of GenBank accession number AF73423.
; OTHER INFORMATION: nbank sequence Accession Number AAF73423.
; PUBLICATION INFORMATION:
; AUTHORS: Nava et al.
; TITLE: Functional characterization of human sphingosine kinase-1
; JOURNAL: FEBS Lett.
; VOLUME: 473
; ISSUE: 1
; PAGES: 81-84
; DATE: 2000
; DATABASE ACCESSION NUMBER: AAF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
; US-09-796-487-3

Query Match 65.1%; Score 250; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 4.9e-235;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAGGPGVLPKPCRVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTMLTERRNHA 60
Db 1 MDPAGGPGVLPKPCRVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTMLTERRNHA 60
Qy 61 RELVRSSELGRWDALVVMGDLMEHVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSELGRWDALVVMGDLMEHVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Qy 121 NHYAGYEQVTNEDLLTNCTLLCRLLSPMNLLSLHTASGLRFLSVLSLAWGFADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCTLLCRLLSPMNLLSLHTASGLRFLSVLSLAWGFADVDLE 180
Qy 181 SEKYRRLGEMRFTGTFLRLAALRYRGLAYLPVGRVSGTKTPASPVVVQGPVDAHLVP 240
Db 181 SEKYRRLGEMRFTGTFLRLAALRYRGLAYLPVGRVSGTKTPASPVVVQGPVDAHLVP 240
Qy 241 LEEPVPSHWT 250
Db 241 LEEPVPSHWT 250

RESULT 7
US-09-205-258-328
; Sequence 328 Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 328
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-328
Query Match 54.4%; Score 209; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-195;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 128 QVTNEDLLTNCILLCRLLSPNLLSIHTASGLRFLSVLSLAWGFADVDLSEKYREL 187
DB 37 QVTNEDLLTNCILLCRLLSPNLLSIHTASGLRFLSVLSLAWGFADVDLSEKYREL 96
QY 188 GEMRFTLGTFLRLAALTYRGLAYLPVGRVSKTPASPVVQOQPVDAHLVPLEPVPVS 247
DB 97 GEMRFTLGTFLRLAALTYRGLAYLPVGRVSKTPASPVVQOQPVDAHLVPLEPVPVS 156
QY 248 HWTVPVDEDFVLVALLHSLGSEMPAAMPGRCAAGVHLYFYVRAGVSRAMLRLFLAME 307
DB 157 HWTVPVDEDFVLVALLHSLGSEMPAAMPGRCAAGVHLYFYVRAGVSRAMLRLFLAME 216
QY 308 KGRHMEYECPLYVYVVPVAFRLPKDGGK 336
DB 217 KGRHMEYECPLYVYVVPVAFRLPKDGGK 245
RESULT 8
US-09-796-487-9
Sequence 9, Application US/09796487
Patent No. 6830916
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09796,487
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 204
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(204)
OTHER INFORMATION: Putative kinase sequence obtained by assembling sequences from several human ESTs (accession numbers D31133, AA232791, W63556, AA026479).
OTHER INFORMATION: Corresponding to peptide sequence Putative Human in Figure 2.
US-09-796-487-9
Query Match 27.9%; Score 107; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.2e-96;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 LNPRGGKGKALQFLFRSHVQPLLAABAEISFTLMLTERRNHARELYRSEELGRWDALVVMVG 80
DB 1 LNPRGGKGKALQFLFRSHVQPLLAABAEISFTLMLTERRNHARELYRSEELGRWDALVVMVG 60
QY 81 DGLMHEVVNGLMERPDWETAIOKPLCPLPAGSGNALAASLNHYAGYE 127
DB 61 DGLMHEVVNGLMERPDWETAIOKPLCPLPAGSGNALAASLNHYAGYE 107
RESULT 9
US-09-205-258-788
Sequence 788, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 788
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (41)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-788

Query Match          14.3%; Score 55; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 LVLLNPRGGKALQLFRSHVQPLIAEAIEISFTLMTERRNHARELVRSSELGRW 72
Db 42 LVLLNPRGGKALQLFRSHVQPLIAEAIEISFTLMTERRNHARELVRSSELGRW 96

RESULT 10
US-09-959-897-13
; Sequence 13, Application US/09959897
; Patent No. 6730480
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/09/959,897
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 788
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-959-897-21
Query Match          8.6%; Score 33; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 109
Db 29 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 61

RESULT 12
US-09-796-487-5
; Sequence 5, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001a (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868

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; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-959-897-13

Query Match          8.6%; Score 33; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 109
Db 29 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 61

RESULT 11
US-09-959-897-21
; Sequence 21, Application US/09959897
; Patent No. 6730480
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/09/959,897
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-959-897-21

Query Match          8.6%; Score 33; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 109
Db 29 VMSGDGLMHVVGVLMERPDWETAIQKPLCSLP 61

RESULT 12
US-09-796-487-5
; Sequence 5, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001a (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868

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; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(373)
;   OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHK1a in Fig. 2, corresponding to amino acid residue 131 to 504 of SPHK1a of GenBank
;   OTHER INFORMATION: sequence Accession Number AAC61697.
; PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AAC61697
;   DATABASE ENTRY DATE: 1998-09-26
;   RELEVANT RESIDUES: (132)..(504)
US-09-796-487-5

Query Match      8.6%; Score 33; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
Db 68 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 100

RESULT 13
US-09-796-487-1
; Sequence 1, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 381
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(381)
;   OTHER INFORMATION: SEQ ID NO 1 is the peptide sequence of mSPHK1a in Figure 1, corresponding to amino acid residue 124 to 504 of SPHK1a of GenBank
;   OTHER INFORMATION: sequence Accession Number AAC61697. SEQ ID NO 1 is equivalent to SEQ ID NO 5
;   OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHK1a in Figure 3.
; PUBLICATION INFORMATION:
;   AUTHORS: Kohama et al.
;   TITLE: Molecular cloning and functional characterization of murine sphingosin kinase
;   JOURNAL: Journal of Biological Chemistry
;   VOLUME: 237
;   ISSUE: 37
;   PAGES: 23722-23782
;   DATE: 1998
;   DATABASE ACCESSION NUMBER: AAC61697
;   DATABASE ENTRY DATE: 1998-09-26
;   RELEVANT RESIDUES: (124)..(504)
; PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AAC61697
;   DATABASE ENTRY DATE: 1998-09-26
;   RELEVANT RESIDUES: (124)..(504)
US-09-796-487-1
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Query Match      8.6%; Score 33; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
Db 76 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 108

RESULT 14
US-09-796-487-4
; Sequence 4, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 381
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(381)
;   OTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of mSPHK1a in Figure 3, corresponding to amino acid residue 124 to 504 of SPHK1a of GenBank
;   OTHER INFORMATION: sequence Accession Number AF068748. SEQ ID NO 4 is equivalent to SEQ ID NO 1
;   OTHER INFORMATION: ID NO 1 that is the amino acid sequence of SPHK1a in Figure 1.
; PUBLICATION INFORMATION:
;   AUTHORS: Kohama et al.
;   TITLE: Molecular cloning and functional characterization of murine sphingosine kinase
;   JOURNAL: Journal of Biological Chemistry
;   VOLUME: 273
;   ISSUE: 37
;   PAGES: 23722-23728
;   DATE: 1998
;   DATABASE ACCESSION NUMBER: AAC61697
;   DATABASE ENTRY DATE: 1998-09-26
;   RELEVANT RESIDUES: (124)..(504)
; PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AAC61697
;   DATABASE ENTRY DATE: 1998-09-26
;   RELEVANT RESIDUES: (124)..(504)
US-09-796-487-4

Query Match      8.6%; Score 33; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
Db 76 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 108

RESULT 15
US-09-970-516-6
; Sequence 6, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of sphingosine kinases
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
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; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-970-516-6

Query Match      8.6%; Score 33; DB 4; Length 382;
Best Local Similarity 100.0%; Pred.No. 1.1e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
Db      77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109

```

Search completed: June 15, 2005, 12:23:31
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 12:11:34 ; Search time 169 Seconds
(without alignments)
1163.541 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 384
Sequence: 1 MDPAGRGVLPKRCVLVL.....CVEPPPSWKPMPPPEPL 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 51207187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	87.5	384	1 SPH1 HUMAN	Q9nval1 homo sapien
2	336	87.5	470	2 Q8N632	Q8n632 homo sapien
3	333	86.7	398	2 Q96GK1	Q96GK1 homo sapien
4	239	62.2	287	2 Q9BTG7	Q9btg7 homo sapien
5	235	61.2	384	2 Q96HV8	Q96hv8 homo sapien
6	125	32.6	329	2 Q9NOA5	Q9n0a5 macaca fasc
7	33	8.6	381	2 Q91ZN3	Q91zn3 mus musculu
8	33	8.6	382	2 Q8C115	Q8c115 mus musculu
9	33	8.6	388	2 Q88886	Q88886 mus musculu
10	33	8.6	504	2 Q88885	Q88885 mus musculu
11	22	5.7	383	2 Q91V26	Q91v26 rattus norv
12	22	5.7	383	2 Q642F6	Q642f6 rattus norv
13	9	2.3	118	2 Q8Y1S2	Q8y1s2 ralstonia s
14	9	2.3	244	2 SPN2M3	Q8n2m3 homo sapien
15	9	2.3	654	1 SPH2 HUMAN	Q9nra0 homo sapien
16	8	2.1	208	2 Q916Y8	Q916y8 pseudomonas
17	8	2.1	292	2 Q7NFU6	Q7nfu6 gloeobacter
18	8	2.1	292	2 Q7VTE9	Q7vte9 bordetella
19	8	2.1	292	2 Q7W5H0	Q7w5h0 bordetella
20	8	2.1	292	2 Q7WD06	Q7wd06 bordetella
21	8	2.1	309	2 Q34799	Q34799 bacillus su
22	8	2.1	327	2 Q87IC1	Q87ic1 vibrio para
23	8	2.1	329	2 Q8BI42	Q8bi42 mus musculu
24	8	2.1	341	2 Q8TAX6	Q8tax6 homo sapien
25	8	2.1	359	2 Q881W7	Q881w7 pseudomonas
26	8	2.1	522	2 Q7MD15	Q7md15 vibrio vuln
27	8	2.1	522	2 Q87FJ5	Q87fj5 vibrio para
28	8	2.1	522	2 Q8D6M6	Q8d6m6 vibrio vuln
29	8	2.1	522	2 Q8E188	Q8e188 shewanella
30	8	2.1	555	1 ROL_MOUSE	Q8r081 mus musculu
31	8	2.1	558	1 ROL_HUMAN	P14866 homo sapien

32	8	2.1	558	2	Q6NTA2	Q6nta2 homo sapien
33	8	2.1	615	2	Q8T3E7	Q8t3e7 caenorhabdi
34	8	2.1	619	2	Q82VG1	Q82vg1 nitrosomona
35	8	2.1	661	2	Q9VZW0	Q9vzw0 drosophila
36	8	2.1	796	2	Q9GYQ9	Q9gyq9 caenorhabdi
37	8	2.1	1088	1	KGP2_DROME	Q3043 drosophila
38	8	2.1	1088	2	Q9VQT2	Q9vqt2 drosophila
39	8	2.1	1168	2	Q7N850	Q7n850 photorhabdu
40	7	1.8	29	2	Q9N2H2	Q9n2h2 bos taurus
41	7	1.8	35	2	Q737L8	Q737l8 bacillus ce
42	7	1.8	45	2	Q80VC3	Q80vc3 mus musculu
43	7	1.8	49	2	Q8IS87	Q8is87 trypanosoma
44	7	1.8	57	2	Q82A09	Q82a09 streptomyc
45	7	1.8	58	2	Q82YB4	Q82yb4 streptomyc
46	7	1.8	59	2	Q9AD30	Q9ad30 streptomyc
47	7	1.8	60	2	Q93J10	Q93ji0 streptomyc
48	7	1.8	62	1	RS27_METJA	P54028 methanococ
49	7	1.8	62	2	Q8ZDT9	Q8zdt9 oryza sativ
50	7	1.8	82	2	Q8XY59	Q8xy59 ralstonia s
51	7	1.8	87	2	Q8U978	Q8u978 agrobacteri
52	7	1.8	89	2	O18200	O18200 caenorhabdi
53	7	1.8	96	2	Q63UF0	Q63uf0 burkholderi
54	7	1.8	97	2	Q7CTG5	Q7ctg5 agrobacteri
55	7	1.8	99	2	Q9AEM7	Q9aem7 bacillus li
56	7	1.8	117	2	Q6UKG2	Q6ukg2 geobacter s
57	7	1.8	117	1	YJV5_YEAST	Q6ukg2 phoronis ps
58	7	1.8	119	1	P90556	P40895 saccharomyc
59	7	1.8	119	2	Q8H615	P90596 trypanosoma
60	7	1.8	119	2	Q9YGD0	Q8h615 oryza sativ
61	7	1.8	119	2	Q8H615	Q9ygd0 petromyzon
62	7	1.8	128	2	Q6ESW0	Q6esw0 oryza sativ
63	7	1.8	128	2	Q9RS8G	Q9rs8g deinococcus
64	7	1.8	130	2	Q74F04	Q74f04 geobacter s
65	7	1.8	130	2	Q6TCF7	Q6tcf7 brachydanio
66	7	1.8	132	2	O26113	O03613 crithidia f
67	7	1.8	135	1	H2A_TRYCR	P30666 trypanosoma
68	7	1.8	135	2	O02617	O02617 trypanosoma
69	7	1.8	135	2	Q8T2X9	Q8t2x9 trypanosoma
70	7	1.8	135	2	Q27794	Q27794 trypanosoma
71	7	1.8	135	2	Q9U701	Q9u701 trypanosoma
72	7	1.8	135	2	Q9U917	Q9u917 trypanosoma
73	7	1.8	138	2	Q7JFY0	Q7jfy0 bos taurus
74	7	1.8	138	2	Q9PSW2	Q9psw2 petromyzon
75	7	1.8	138	2	Q9PSW3	Q9psw3 petromyzon
76	7	1.8	139	1	LAMP_PETWA	P33575 petromyzon
77	7	1.8	144	2	Q6K5Y3	Q6k5y3 oryza sativ
78	7	1.8	147	2	Q73MK3	Q73mk3 treponema d
79	7	1.8	148	2	Q8VQH7	Q8vqh7 uncultured
80	7	1.8	153	2	O69604	O69604 methylobact
81	7	1.8	154	2	Q82GA6	Q82ga6 streptomyc
82	7	1.8	156	2	Q985U3	Q985u3 rhizobium l
83	7	1.8	156	2	Q6P394	Q6p394 mus musculu
84	7	1.8	157	2	Q6P0W6	Q6p0w6 mus musculu
85	7	1.8	160	2	Q6NHV2	Q6nhv2 corynebacte
86	7	1.8	166	2	Q24864	Q24864 entamoeba h
87	7	1.8	167	2	Q8BHX5	Q8bhx5 mus musculu
88	7	1.8	168	2	Q7P0T5	Q7p0t5 chromobacte
89	7	1.8	184	2	Q966Y2	Q966y2 suberites d
90	7	1.8	184	2	Q6D119	Q6d119 erwinia car
91	7	1.8	185	2	Q8Q15	Q8q15 streptococc
92	7	1.8	185	2	Q97RQ5	Q97rq5 streptococc
93	7	1.8	191	2	Q8PXF1	Q8pxf1 methanosaar
94	7	1.8	193	2	Q911G3	Q91lg3 pseudomonas
95	7	1.8	194	2	Q6D475	Q6d475 erwinia car
96	7	1.8	195	2	Q9UEF8	Q9uef8 homo sapien
97	7	1.8	203	2	Q72T67	Q72t67 leptospira
98	7	1.8	203	2	Q8F282	Q8fvk2 leptospira
99	7	1.8	204	1	COAE_RALSO	Q8ndr1 homo sapien
100	7	1.8	205	2	Q8NDE1	Q8ndr1 homo sapien
101	7	1.8	206	2	Q87BP3	Q87bp3 xylalla fas
102	7	1.8	207	2	Q6N6K8	Q6n6k8 rhodopseudo
103	7	1.8	210	2	Q95SL8	Q95sl8 drosophila
104	7	1.8	210	2	Q9W3R3	Q9w3r3 drosophila

105	7	1.8	211	2	Q6MLF4	Q6mlf4 bdellovibri	178	7	1.8	299	2	Q9UEB9	Q9uee9 homo sapien
106	7	1.8	211	2	Q9JRM6	Q9jrm6 mus musculus	179	7	1.8	304	2	Q73KV6	Q73kv6 treponema d
107	7	1.8	212	2	Q6XFA4	Q6xf4 actinobacil	180	7	1.8	305	2	Q9XVA7	Q9xva7 caenorhabdi
108	7	1.8	212	2	Q6XFA9	Q6xf9 actinobacil	181	7	1.8	305	2	Q6KIQ1	Q6kiq1 mycoplasma
109	7	1.8	212	2	P74511	P74511 synechocyst	182	7	1.8	306	2	Q8Y497	Q8y497 listeria mo
110	7	1.8	212	2	Q880R5	Q880r5 pseudomonas	183	7	1.8	306	2	Q927T6	Q927t6 listeria in
111	7	1.8	214	2	Q9ZFL5	Q9zfl5 bacillus st	184	7	1.8	306	2	Q71WM2	Q71wm2 listeria mo
112	7	1.8	215	2	Q81031	Q81031 bos taurus	185	7	1.8	307	2	Q82FR6	Q82fr6 streptomyce
113	7	1.8	215	2	Q8H1H2	Q8h1h2 lycopersico	186	7	1.8	308	2	Q6SW11	Q6sw11 human cytom
114	7	1.8	217	2	Q00404	Q00404 homo sapien	187	7	1.8	308	2	Q6SW18	Q6sw18 human cytom
115	7	1.8	217	2	Q7X1F5	Q7x1f5 leptospiril	188	7	1.8	308	2	Q6SWK2	Q6swk2 human cytom
116	7	1.8	219	2	Q73UF4	Q73uf4 mycobacteri	189	7	1.8	308	2	Q6SMW9	Q6smw9 human cytom
117	7	1.8	221	2	Q66AH6	Q66ah6 yersinia ps	190	7	1.8	308	2	Q6SMW7	Q6smw7 human cytom
118	7	1.8	221	2	Q7E180	Q7e180 actinobacil	191	7	1.8	308	2	Q6SWT5	Q6swt5 human cytom
119	7	1.8	221	2	Q65KU3	Q65ku3 bacillus li	192	7	1.8	308	2	Q6SWZ2	Q6swz2 human cytom
120	7	1.8	221	2	P96900	P96900 mycobacteri	193	7	1.8	308	2	Q6SX21	Q6sx21 human cytom
121	7	1.8	221	2	Q8ZEEL	Q8zeel yersinia pe	194	7	1.8	311	2	Q86JS6	Q86js6 dictyosteli
122	7	1.8	221	2	Q7TWS9	Q7tws9 mycobacteri	195	7	1.8	312	1	QXYR_STRVD	Q9x5p2 streptomyce
123	7	1.8	222	2	Q62MK5	Q62mk5 burkholderi	196	7	1.8	312	2	Q6A7L4	Q6a7l4 propionibac
124	7	1.8	222	2	Q63X60	Q63x60 burkholderi	197	7	1.8	312	2	Q9FBP4	Q9fbp4 streptomyce
125	7	1.8	223	2	Q9CCL4	Q9cc14 mycobacteri	198	7	1.8	313	2	Q9RN71	Q9rn71 streptomyce
126	7	1.8	225	2	Q69S39	Q69s39 oryza sativ	199	7	1.8	313	2	Q9ZBG5	Q9zbg5 streptomyce
127	7	1.8	225	2	Q9ZSU7	Q9zsu7 oryza sativ	200	7	1.8	314	2	Q7W5L1	Q7w5l1 bordetella
128	7	1.8	225	2	Q6P7V8	Q6p7v8 xenopus tro	201	7	1.8	314	2	Q7WD47	Q7wd47 bordetella
129	7	1.8	230	2	Q89E09	Q89e09 bradyrhizob	202	7	1.8	315	2	Q88H04	Q88h04 pseudomonas
130	7	1.8	232	2	Q6SFF6	Q6sf68 uncultured	203	7	1.8	317	2	Q7VW53	Q7vw53 bordetella
131	7	1.8	233	2	Q98FR1	Q98fr1 rhizobium l	204	7	1.8	318	2	Q9ADM4	Q9adm4 streptomyce
132	7	1.8	238	2	Q65967	Q65967 cucurbit ap	205	7	1.8	319	2	Q8Y2S7	Q8y2s7 talistonia s
133	7	1.8	239	2	Q9XH21	Q9xh21 arabidopsis	206	7	1.8	320	2	Q70PA0	Q70pa0 melittangiu
134	7	1.8	242	2	Q6YKFL	Q6ykf1 aphodius wi	207	7	1.8	323	2	Q6I859	Q6i859 aeromicrobi
135	7	1.8	242	2	Q49662	Q49662 mycobacteri	208	7	1.8	324	2	Q9SSE9	Q9sse9 synechoccc
136	7	1.8	242	2	Q98J99	Q98j99 rhizobium l	209	7	1.8	324	2	Q748R4	Q748r4 geobacter s
137	7	1.8	244	2	Q7XJH6	Q7xjh6 sairocarpus	210	7	1.8	324	2	Q89HC2	Q89hc2 bradyrhizob
138	7	1.8	245	1	H1S4_PSEAE	Q9hu43 pseudomonas	211	7	1.8	326	2	Q63U07	Q63u07 burkholderi
139	7	1.8	248	2	Q8LNG3	Q8lng3 oryza sativ	212	7	1.8	328	2	Q68387	Q68387 human cytom
140	7	1.8	249	2	Q6AF21	Q6afz1 leifsonia x	213	7	1.8	328	2	Q64ER1	Q64er1 human cytom
141	7	1.8	254	2	Q8TVL3	Q8tv13 methanopyru	214	7	1.8	328	2	Q64ER4	Q64er4 human cytom
142	7	1.8	254	2	Q88GV7	Q88gv7 pseudomonas	215	7	1.8	328	2	Q64ER5	Q64er5 human cytom
143	7	1.8	255	2	Q93V74	Q93v74 arabidopsis	216	7	1.8	328	2	Q64ER6	Q64er6 human cytom
144	7	1.8	257	2	Q9HU49	Q9hu49 pseudomonas	217	7	1.8	328	2	Q64ER7	Q64er7 human cytom
145	7	1.8	257	2	Q6NW92	Q6nw92 brachydanio	218	7	1.8	328	2	Q64ER9	Q64er9 human cytom
146	7	1.8	263	2	Q7Y125	Q7y125 antirrhinum	219	7	1.8	328	2	Q64ES0	Q64es0 human cytom
147	7	1.8	264	2	Q7Y126	Q7y126 antirrhinum	220	7	1.8	328	2	Q64ES1	Q64es1 human cytom
148	7	1.8	265	2	Q74TU6	Q74tu6 yersinia pe	221	7	1.8	328	2	Q64ES3	Q64es3 human cytom
149	7	1.8	265	2	Q8D0J1	Q8d0j1 yersinia pe	222	7	1.8	328	2	Q64ES4	Q64es4 human cytom
150	7	1.8	266	2	Q7Y118	Q7y118 mohavea con	223	7	1.8	328	2	Q64ES5	Q64es5 human cytom
151	7	1.8	266	2	Q7Y119	Q7y119 antirrhinum	224	7	1.8	328	2	Q64ES8	Q64es8 human cytom
152	7	1.8	266	2	Q7Y120	Q7y120 antirrhinum	225	7	1.8	328	2	Q64ES9	Q64es9 human cytom
153	7	1.8	266	2	Q7Y121	Q7y121 antirrhinum	226	7	1.8	328	2	Q64ET0	Q64et0 human cytom
154	7	1.8	266	2	Q7Y122	Q7y122 antirrhinum	227	7	1.8	328	2	Q64ET2	Q64et2 human cytom
155	7	1.8	266	2	Q7Y123	Q7y123 sairocarpus	228	7	1.8	328	2	Q64ET3	Q64et3 human cytom
156	7	1.8	266	2	Q6D253	Q6d253 erwinia car	229	7	1.8	328	2	Q64ET4	Q64et4 human cytom
157	7	1.8	267	2	Q6N7T5	Q6n7t5 rhodopseudo	230	7	1.8	334	1	RUVB_THEME	Q56313 thermotoga
158	7	1.8	268	2	Q97GM1	Q97gm1 clostridium	231	7	1.8	334	2	Q6UUK1	Q6uuk1 oryza sativ
159	7	1.8	275	2	Q63N11	Q63ni1 burkholderi	232	7	1.8	335	2	Q6Z1B6	Q6z1b6 oryza sativ
160	7	1.8	277	2	Q00393	Q00393 homo sapien	233	7	1.8	336	2	Q82IC7	Q82ic7 streptomyce
161	7	1.8	277	2	Q8C1C5	Q8c1c5 mus musculu	234	7	1.8	338	2	Q6ZT29	Q6zt29 homo sapien
162	7	1.8	280	2	P71054	P71054 bacillus su	235	7	1.8	338	2	P91027	P91027 caenorhabdi
163	7	1.8	282	2	Q65EK4	Q65ek4 bacillus li	236	7	1.8	342	2	Q828U6	Q828u6 streptomyce
164	7	1.8	281	2	Q867A5	Q867a5 tragulus ja	237	7	1.8	346	2	Q6K7A7	Q6k7a7 oryza sativ
165	7	1.8	281	2	Q8S5N4	Q8s5n4 oryza sativ	238	7	1.8	346	2	Q6NRH7	Q6nrh7 xenopus lae
166	7	1.8	281	2	Q82LS3	Q82ls3 streptomyce	239	7	1.8	348	2	Q82MG5	Q82mg5 streptomyce
167	7	1.8	283	2	Q9RJF9	Q9rjf9 streptomyce	240	7	1.8	348	2	Q6PC40	Q6pc40 brachydanio
168	7	1.8	285	1	RM01_YEAST	Q04599 saccharomyc	241	7	1.8	351	2	Q9S3V4	Q9s3v4 cellulomona
169	7	1.8	286	2	Q74D29	Q74d29 geobacter s	242	7	1.8	352	2	Q9UVZ0	Q9uvz0 pyrenopeziz
170	7	1.8	287	2	Q6P7H7	Q6p7h7 xenopus lae	243	7	1.8	352	2	Q49487	Q49487 arabidopsis
171	7	1.8	288	2	Q840X5	Q840x5 streptomyce	244	7	1.8	352	2	Q9X3L7	Q9x3l7 streptomyce
172	7	1.8	288	2	Q98M46	Q98m46 rhizobium l	245	7	1.8	355	2	Q8GR76	Q8gr76 rhodovulum
173	7	1.8	292	2	Q9X9X2	Q9x9x2 streptomyce	246	7	1.8	356	2	Q8ZT08	Q8zt08 pyrobaculum
174	7	1.8	294	2	Q69YM6	Q69ym6 homo sapien	247	7	1.8	358	2	Q00518	Q00518 mycobacteri
175	7	1.8	296	2	Q65HJ1	Q65hj1 bacillus li	248	7	1.8	358	2	Q7U105	Q7u105 mycobacteri
176	7	1.8	297	2	Q8HXY9	Q8hxy9 bos taurus	249	7	1.8	359	2	Q6BCL3	Q6bcl3 bursaphelen
177	7	1.8	298	2	Q9ESA9	Q9esa9 rattus norv	250	7	1.8	359	2	Q90351	Q90351 coturnix co

251	7	1.8	360	2	Q8G1Q4	Q8G1Q4 streptomyc	324	7	1.8	453	2	Q54309	Q54309 streptomyc
252	7	1.8	364	2	Q727F1	Q727f1 deulfovibr	325	7	1.8	453	2	Q12945	Q12945 gallus gall
253	7	1.8	365	2	Q7Q262	Q7q262 anopheles g	326	7	1.8	457	2	Q7A71	Q7a71 thermoplaam
254	7	1.8	365	2	Q8FJL1	Q8fjl1 xanthomonas	327	7	1.8	457	2	Q6FKM9	Q6fkm9 candida gla
255	7	1.8	367	2	Q94DX5	Q94dx5 oryza sativ	328	7	1.8	457	2	Q8MNS2	Q8mns2 caenorhabdi
256	7	1.8	368	2	Q7RW14	Q7rw14 neurospora	329	7	1.8	458	2	Q6GEA8	Q6gea8 staphylococ
257	7	1.8	369	2	Q8N8M0	Q8nm80 homo sapien	330	7	1.8	459	2	Q8NV69	Q8nv69 staphylococ
258	7	1.8	369	2	Q9JXZ8	Q9jxz8 neisseria m	331	7	1.8	459	2	Q7A327	Q7a327 staphylococ
259	7	1.8	371	2	Q6N342	Q6n342 rhodopsendo	332	7	1.8	459	2	Q82W37	Q82w37 nitrosomona
260	7	1.8	372	2	Q8P862	Q8p862 xanthomonas	333	7	1.8	459	2	Q6G6Z4	Q6g6z4 staphylococ
261	7	1.8	372	2	Q7VDR7	Q7vdr7 prochlorococ	334	7	1.8	461	2	Q3S947	Q3s947 mesocricetu
262	7	1.8	373	2	Q84GM4	Q84gm4 xanthomonas	335	7	1.8	462	2	Q7M9V9	Q7m9v9 wolinnella s
263	7	1.8	373	2	Q83NC6	Q83nc6 bradyrhizob	336	7	1.8	463	2	Q73S19	Q73s19 mycobacteri
264	7	1.8	378	2	Q6FTH2	Q6fth2 candida gla	337	7	1.8	470	2	Q732Q3	Q732q3 mus musculu
265	7	1.8	378	2	Q7V325	Q7v325 prochlorococ	338	7	1.8	472	1	MMGE_BACSU	MMGE_BACSU
266	7	1.8	379	2	Q9C1M3	Q9c1m3 emericella	339	7	1.8	473	2	Q6C700	Q6c700 yarrowia li
267	7	1.8	380	2	Q744E7	Q744e7 mycobacteri	340	7	1.8	476	2	Q8E1S6	Q8e1s6 streptococ
268	7	1.8	382	2	Q54173	Q54173 streptomyc	341	7	1.8	476	2	Q8E790	Q8e790 streptococ
269	7	1.8	384	2	Q8WZH0	Q8wzh0 coccidioid	342	7	1.8	476	2	Q57174	Q57174 vaccinia vi
270	7	1.8	385	2	Q9PFR8	Q9pfr8 xylella fas	343	7	1.8	478	2	Q54231	Q54231 streptococ
271	7	1.8	385	2	Q7TMJ5	Q7tmj5 mus musculu	344	7	1.8	485	2	Q6CAN8	Q6can8 yarrowia li
272	7	1.8	387	2	Q69XQ6	Q69xq6 oryza sativ	345	7	1.8	487	2	Q7PXA6	Q7pxa6 anopheles g
273	7	1.8	389	2	Q9AD61	Q9ad61 streptomyc	346	7	1.8	488	2	Q7X791	Q7x791 oryza sativ
274	7	1.8	390	2	Q7V4T3	Q7v4t3 prochlorococ	347	7	1.8	488	2	Q8PEP4	Q8pep4 xanthomonas
275	7	1.8	393	2	Q84J13	Q84j13 pleurocappa	348	7	1.8	490	2	Q6T6X7	Q6t6x7 pellona fla
276	7	1.8	395	2	Q84J16	Q84j16 xenococcus	349	7	1.8	491	2	Q6T6W9	Q6t6w9 thymallus t
277	7	1.8	396	2	Q7X4A3	Q7x4a3 hapalosiph	350	7	1.8	492	1	AMPA_SYN3	AMPA_SYN3
278	7	1.8	396	2	Q7X4A4	Q7x4a4 hapalosiph	351	7	1.8	492	1	Y3D9_BACHD	Y3D9_BACHD
279	7	1.8	396	2	Q7X4A5	Q7x4a5 chlorogloeo	352	7	1.8	496	1	GRB_MOUSE	GRB_MOUSE
280	7	1.8	396	2	Q7X4A6	Q7x4a6 fischerella	353	7	1.8	496	1	GRB_RAT	GRB_RAT
281	7	1.8	396	2	Q7X4A7	Q7x4a7 nostoc ento	354	7	1.8	496	2	Q8BLF5	Q8blf5 mus musculu
282	7	1.8	396	2	Q7X4A8	Q7x4a8 tollyporthix	355	7	1.8	497	1	GRB_HUMAN	GRB_HUMAN
283	7	1.8	396	2	Q7X4A9	Q7x4a9 anabaena pl	356	7	1.8	497	2	Q6KEX4	Q6kex4 sus scrofa
284	7	1.8	396	2	Q84J10	Q84j10 chroococcid	357	7	1.8	497	2	Q6GJS9	Q6gjs9 bos taurus
285	7	1.8	396	2	Q84J14	Q84j14 nodularia s	358	7	1.8	499	2	Q7XRZ6	Q7xrz6 oryza sativ
286	7	1.8	396	2	Q84J15	Q84j15 fischerella	359	7	1.8	499	2	Q8K669	Q8k669 streptococ
287	7	1.8	396	2	Q84J18	Q84j18 chlorogloeo	360	7	1.8	499	2	Q8NZX3	Q8nzx3 streptococ
288	7	1.8	396	2	Q84J24	Q84j24 anabaena va	361	7	1.8	499	2	Q99YJ1	Q99yj1 streptococ
289	7	1.8	396	2	Q84J26	Q84j26 anabaena cy	362	7	1.8	501	2	Q96Q09	Q96q09 drosophila
290	7	1.8	396	2	Q84J27	Q84j27 nostoc linc	363	7	1.8	502	2	Q7PY56	Q7py56 anopheles g
291	7	1.8	396	2	Q84J30	Q84j30 anabaena va	364	7	1.8	506	2	Q6Z7C0	Q6z7c0 oryza sativ
292	7	1.8	396	2	Q84J30	Q84j30 anabaenopsi	365	7	1.8	508	1	HUTH_BACSU	HUTH_BACSU
293	7	1.8	398	2	Q84J28	Q84j28 calothrix b	366	7	1.8	508	2	Q6PPY9	Q6ppy9 magnetite-c
294	7	1.8	399	1	PNB1_PSEAE	PNB1_PSEAE	367	7	1.8	515	2	Q6BWE2	Q6bwe2 debaryomyce
295	7	1.8	399	1	SHBG_PROSU	SHBG_PROSU	368	7	1.8	515	2	Q7E910	Q7e910 drosophila
296	7	1.8	400	2	Q9X7S6	Q9x7s6 streptomyc	369	7	1.8	518	2	Q6UIR3	Q6uir3 salvelinus
297	7	1.8	402	2	Q9WZK6	Q9wzk6 thermotoga	370	7	1.8	518	2	Q6UIR3	Q6uir3 anopheles g
298	7	1.8	403	2	Q9AE01	Q9ae01 amycolatops	371	7	1.8	518	2	Q7PRQ4	Q7prq4 anopheles g
299	7	1.8	410	1	METK_CORDI	METK_CORDI	372	7	1.8	525	2	Q7PZS8	Q7pzs8 anopheles g
300	7	1.8	411	2	Q9F5I9	Q9f5i9 escherichia	373	7	1.8	527	2	Q9A4B7	Q9a4b7 caulobacter
301	7	1.8	411	2	Q6U9Y5	Q6u9y5 thalassiosol	374	7	1.8	529	2	Q8WUL6	Q8wul6 homo sapien
302	7	1.8	414	2	Q6U9Y5	Q6u9y5 thalassiosol	375	7	1.8	536	2	Q917H9	Q917h9 drosophila
303	7	1.8	420	1	PSD4_SCHMA	PSD4_SCHMA	376	7	1.8	537	2	Q945B8	Q945b8 euphorbia e
304	7	1.8	420	1	EPC_MOUSE	EPC_MOUSE	377	7	1.8	538	2	Q945B9	Q945b9 euphorbia e
305	7	1.8	421	1	SYH_CORHU	SYH_CORHU	378	7	1.8	540	2	Q7UE48	Q7ue48 rhodopirell
306	7	1.8	422	1	Q8FRS1	Q8frs1 corynebacte	379	7	1.8	540	2	Q7M858	Q7m858 novinnella s
307	7	1.8	422	1	Q8FRS1	Q8frs1 corynebacte	380	7	1.8	543	2	Q6UIQ2	Q6uiq2 novinnella s
308	7	1.8	426	1	Q9RFE8	Q9rfe8 rhodobacter	381	7	1.8	545	2	Q6UIQ8	Q6uiq8 dallia pect
309	7	1.8	428	1	FOLC_LACCA	FOLC_LACCA	382	7	1.8	546	2	Q6UIQ3	Q6uiq3 esox reiche
310	7	1.8	429	2	Q8GAH1	Q8gah1 arthrobacte	383	7	1.8	546	2	Q6UIQ4	Q6uiq4 esox niger
311	7	1.8	434	1	PURA_CAEEL	PURA_CAEEL	384	7	1.8	546	2	Q6UIQ5	Q6uiq5 esox masqui
312	7	1.8	438	2	Q64S50	Q64s50 bacteroides	385	7	1.8	546	2	Q6UIQ6	Q6uiq6 esox lucius
313	7	1.8	440	2	Q9KXP0	Q9kpx0 vibrio chol	386	7	1.8	547	2	Q6SL27	Q6sl27 argulus ame
314	7	1.8	442	2	Q83CU4	Q83cu4 coxiella bu	387	7	1.8	552	2	Q8YR42	Q8yr42 anabaena ep
315	7	1.8	442	2	Q9J2J8	Q9j2j8 rheus monk	388	7	1.8	554	1	HUTU_STRAW	HUTU_STRAW
316	7	1.8	442	2	Q9WRP5	Q9wrp5 macaca mulla	389	7	1.8	559	2	Q6MB30	Q6mb30 brachlamyid
317	7	1.8	443	2	Q75DQ5	Q75dq5 ashbya goss	390	7	1.8	567	2	Q89P14	Q89p14 bradyrhizob
318	7	1.8	445	2	Q7X8V1	Q7x8v1 oryza sativ	391	7	1.8	569	2	Q7NKM7	Q7nkm7 gloebacter
319	7	1.8	447	2	Q7QJP7	Q7qjp7 anopheles g	392	7	1.8	569	2	Q7VJM3	Q7vjm3 bordetella
320	7	1.8	449	2	Q91754	Q91754 pseudomonas	393	7	1.8	569	2	Q7W130	Q7w130 bordetella
321	7	1.8	450	2	Q827K9	Q827k9 streptomyc	394	7	1.8	569	2	Q7WNS0	Q7wns0 bordetella
322	7	1.8	450	2	Q6E127	Q6e127 mesoplasma	395	7	1.8	571	2	Q8V7Y8	Q8v7y8 listeria mo
323	7	1.8	453	2	Q97VM1	Q97vm1 sulfolobus	396	7	1.8	571	2		

397	7	1.8	571	2	Q92CS4	Q92cs4	listeria in	470	7	1.8	782	1	PRTP_TUHV2	Q9wrl6	tupaiid her
398	7	1.8	571	2	Q720V1	Q720v1	listeria mo	471	7	1.8	782	2	Q9ES5	Q9esa5	rattus norv
399	7	1.8	574	1	ME22_SCHPO	O60170	schizosacch	472	7	1.8	782	2	Q77L98	Q77l98	tupaiid her
400	7	1.8	574	2	Q75S81	O61070	tragulus ja	473	7	1.8	808	1	PML_MOUSE	Q60953	mus musculu
401	7	1.8	576	2	Q74P57	Q74p57	bacillus ce	474	7	1.8	808	2	Q8VCC4	Q8vcc4	mus musculu
402	7	1.8	578	2	Q6CA63	O6ca63	yarrowia li	475	7	1.8	809	2	Q9A7N2	Q9a7n2	caulobacter
403	7	1.8	583	2	Q8P6L0	O6f610	acinetobact	476	7	1.8	810	2	Q8BUA6	Q8bua6	mus musculu
404	7	1.8	586	2	Q8X7R9	Q8x7r9	escherichia	477	7	1.8	811	2	Q6GI08	Q6g1q8	bartonella
405	7	1.8	588	2	Q8D509	Q8d509	vibrio vuln	478	7	1.8	823	2	Q7RZ35	Q7rz35	neurospora
406	7	1.8	589	2	Q90YL3	Q90yl3	brachydanio	479	7	1.8	841	2	Q63HK2	Q63hk2	homo sapien
407	7	1.8	589	2	Q7ZVI4	Q7zvi4	brachydanio	480	7	1.8	841	2	Q6QCX7	Q6qcx7	trypanosoma
408	7	1.8	590	2	Q82BL5	Q82bl5	streptomyce	481	7	1.8	874	1	CPHA_SYN8	P56947	synecocyst
409	7	1.8	592	2	Q02751	O02751	bos taurus	482	7	1.8	882	1	Y890_MYCTU	Q10550	mycobacteri
410	7	1.8	592	2	Q8I032	Q8i032	bos taurus	483	7	1.8	882	1	Y914_MYCBO	P59969	mycobacteri
411	7	1.8	603	2	Q8HNR2	Q8hnr2	homo sapien	484	7	1.8	882	2	Q7SAC4	Q7sac4	neurospora
412	7	1.8	603	2	Q7MBT8	Q7mbt8	vibrio vuln	485	7	1.8	885	2	Q8CEJ1	Q8cej1	mus musculu
413	7	1.8	603	2	Q7WAN3	Q7wan3	bordeitella	486	7	1.8	891	2	Q7VQG3	Q7vqg3	canidatus
414	7	1.8	605	2	Q7WJT6	Q7wtj6	bordeitella	487	7	1.8	896	2	Q9F2I7	Q9f2i7	synecococc
415	7	1.8	608	2	Q8D5U9	Q8dsu9	vibrio vuln	488	7	1.8	901	1	CPHA_ANASP	P58572	anabaena sp
416	7	1.8	610	2	Q9T6W2	Q9t6w2	cissampelos	489	7	1.8	901	1	CPHA_ANAVA	Q86109	anabaena va
417	7	1.8	613	2	Q8TPP0	Q8tpp0	methanosarc	490	7	1.8	903	2	Q8VTA5	Q8vta5	synecococc
418	7	1.8	615	2	Q7N2J7	Q7n2j7	photorhabdu	491	7	1.8	909	2	Q841L9	Q841l9	streptomyce
419	7	1.8	615	2	Q8E139	Q8e139	shewanella	492	7	1.8	921	2	Q48411	Q48411	klebsiella
420	7	1.8	616	2	Q87FE8	Q87fe8	vibrio para	493	7	1.8	930	2	Q8S8G8	Q8s8g8	arabidopsis
421	7	1.8	616	2	Q8AYB2	Q8ayb2	rattus norv	494	7	1.8	933	2	Q8SHL7	Q8shl7	arabidopsis
422	7	1.8	617	1	SPH2_MOUSE	Q9jia7	mus musculu	495	7	1.8	948	2	Q9KPD4	Q9kpd4	vibrio chol
423	7	1.8	620	2	Q7VWR3	Q7vwr3	bordeitella	496	7	1.8	949	2	O57149	Q571j4	human herpe
424	7	1.8	621	2	Q9LKN9	Q9lnk9	arabidopsis	497	7	1.8	963	2	Q72J34	Q72jj4	thermus the
425	7	1.8	623	2	Q7MCW8	Q7mcw8	vibrio vuln	498	7	1.8	988	2	Q98GK8	Q98gk8	rhizobium l
426	7	1.8	627	2	Q8C7J5	Q8c7j5	mus musculu	499	7	1.8	996	2	Q9A2M0	Q9a2m0	caulobacter
427	7	1.8	629	2	Q62A37	Q62a37	burkholderi	500	7	1.8	998	2	Q7Z5Y3	Q7z5y3	homo sapien
428	7	1.8	629	2	Q3NXX0	Q63nx0	burkholderi	501	7	1.8	1000	2	Q63HR7	Q63hr7	homo sapien
429	7	1.8	632	2	Q7XFC1	Q7xfc1	oryza sativ	502	7	1.8	1001	2	Q9VFA8	Q9vfa8	drosophila
430	7	1.8	632	2	Q3AUP4	Q9aup4	oryza sativ	503	7	1.8	1028	2	Q752Q2	Q752q2	ashbya goss
431	7	1.8	635	2	Q6IP55	Q6ip55	xenopus lae	504	7	1.8	1029	2	Q9YMX0	Q9ymx0	lymantria d
432	7	1.8	636	2	Q3PAP9	Q6paf9	xenopus lae	505	7	1.8	1064	2	Q6P7W6	Q6p7w6	mus musculu
433	7	1.8	638	1	HTPG_STRCO	P58481	streptomyce	506	7	1.8	1066	2	Q7QRV1	Q7qrv1	giardia lam
434	7	1.8	645	2	Q9YLN3	Q8yln3	anabaena sp	507	7	1.8	1080	1	UBP8_MOUSE	Q80u87	mus musculu
435	7	1.8	645	2	Q9FBT3	Q9fbt3	streptomyce	508	7	1.8	1098	2	Q6TFZ6	Q6tfz6	homo sapien
436	7	1.8	645	2	Q6DR98	Q6dr98	mus musculu	509	7	1.8	1103	2	Q9VY72	Q9vy72	drosophila
437	7	1.8	648	2	Q64WT0	Q64wt0	bacteroides	510	7	1.8	1105	2	O8NIA3	Q8nia3	homo sapien
438	7	1.8	653	2	Q95YJ5	Q95yj5	ciona intes	511	7	1.8	1116	2	Q95NI8	Q95ni8	drosophila
439	7	1.8	654	2	Q873H9	O873h9	neurospora	512	7	1.8	1116	2	Q9VM48	Q9vm48	drosophila
440	7	1.8	654	2	Q8P4Y6	Q8p4y6	xenopus tro	513	7	1.8	1122	2	Q960V3	Q960v3	drosophila
441	7	1.8	655	2	Q8L280	Q8l280	proteus vul	514	7	1.8	1122	2	Q7XME6	Q7xme6	oryza sativ
442	7	1.8	655	2	Q7TFJ9	Q7tfj9	rhesus cyto	515	7	1.8	1143	2	O6MAW0	Q6maw0	parachlamyd
443	7	1.8	657	2	Q9SS38	Q9ss38	arabidopsis	516	7	1.8	1149	2	Q9FHN1	Q9fhn1	arabidopsis
444	7	1.8	659	2	Q9FTX1	Q9ftx1	oryza sativ	517	7	1.8	1186	2	O6NXH6	Q6nxh6	mus musculu
445	7	1.8	662	1	NRG1_RAT	P43322	r-pro-neure	518	7	1.8	1207	1	AT19_HUMAN	Q8te59	homo sapien
446	7	1.8	664	2	Q6LKN3	Q6lkn3	photobacter	519	7	1.8	1225	2	Q7ZAP2	Q7zap2	bifidobacte
447	7	1.8	669	2	Q6L1S1	Q6l1s1	streptomyce	520	7	1.8	1239	2	Q9FRS3	Q9frs3	arabidopsis
448	7	1.8	677	2	Q938N2	Q938n2	enterococcu	521	7	1.8	1243	2	O67JD3	Q67jd3	symbiodacte
449	7	1.8	679	2	Q6C335	Q6c335	yarrowia li	522	7	1.8	1253	2	P91601	P91601	calliphora
450	7	1.8	683	2	Q63564	Q63564	rattus norv	523	7	1.8	1253	2	Q23810	Q23810	calliphora
451	7	1.8	689	2	Q8CGE2	O8cge2	mus musculu	524	7	1.8	1289	2	Q93IR7	Q93ir7	salmonella
452	7	1.8	693	2	Q7XV75	Q7xv75	oryza sativ	525	7	1.8	1289	2	Q8ZRL2	Q8zrl2	salmonella
453	7	1.8	694	2	Q5ZV12	Q9zv12	arabidopsis	526	7	1.8	1292	2	Q6ZQL2	Q6zql2	mus musculu
454	7	1.8	694	2	Q7TN62	Q7tn62	mus musculu	527	7	1.8	1297	1	IRR_HUMAN	P14616	homo sapien
455	7	1.8	694	2	Q7TQ65	Q7tq65	mus musculu	528	7	1.8	1300	1	IRR_CAVPO	P14617	cavia porce
456	7	1.8	695	2	Q9ESB0	Q9esb0	rattus norv	529	7	1.8	1300	1	IRR_MOUSE	Q9wt14	mus musculu
457	7	1.8	700	2	Q6DR99	Q6dr99	mus musculu	530	7	1.8	1302	2	Q9W4T8	Q9w4t8	drosophila
458	7	1.8	700	2	Q9ESB1	Q9esb1	rattus norv	531	7	1.8	1305	2	Q80YF9	Q80yf9	mus musculu
459	7	1.8	708	2	Q8L7R6	Q8l7t6	arabidopsis	532	7	1.8	1306	2	O77273	Q77273	drosophila
460	7	1.8	711	2	O88679	O88679	cricetus	533	7	1.8	1308	2	Q9GPM8	Q9gpm8	caenorhabdi
461	7	1.8	713	2	Q8G8J7	Q8g8j7	pseudomonas	534	7	1.8	1319	1	SOS1_MOUSE	Q62245	mus musculu
462	7	1.8	720	2	Q8N6M6	Q8n6m6	homo sapien	535	7	1.8	1320	2	O89VI3	Q89yi3	bacteroides
463	7	1.8	732	2	Q94BZ7	Q94bz7	arabidopsis	536	7	1.8	1333	1	SOS1_HUMAN	Q77889	homo sapien
464	7	1.8	733	2	Q93YGS	Q93yg5	streptococc	537	7	1.8	1357	2	YJ03_YEAST	P47104	saccharomyc
465	7	1.8	743	2	Q8K647	Q8k647	streptococc	538	7	1.8	1370	2	Q6C375	Q6c375	yarrowia li
466	7	1.8	758	2	Q8NZV1	Q8nzv1	streptococc	539	7	1.8	1370	2	Q9DD34	Q9dd34	fugu rubrip
467	7	1.8	760	1	CO2_MOUSE	P21180	mus musculu	540	7	1.8	1390	1	N155_RAT	P37199	rattus norv
468	7	1.8	760	2	Q9FYE7	Q9fye7	arabidopsis	541	7	1.8	1391	1	N155_HUMAN	Q75694	homo sapien
469	7	1.8	760	2	O70350	O70350	mus musculu	542	7	1.8	1391	1	N155_MOUSE	Q99p88	mus musculu

689	6	1.6	84	2	Q89HT2	Q89ht2 bradyrhizob	762	6	1.6	102	2	Q84AZ8	Q84az8 uncultured
690	6	1.6	84	2	Q8VBES	Q8vbes white spot	763	6	1.6	102	2	Q88GZ4	Q88gz4 pseudomonas
691	6	1.6	84	2	Q6PBB6	Q6pbb6 xenopus lae	764	6	1.6	102	2	Q9CCRO	Q9ccro mycobacteri
692	6	1.6	85	2	Q8TPV1	Q8tpv1 methanopyru	765	6	1.6	102	2	Q9D3E0	Q9d3e0 mus musculu
693	6	1.6	85	2	Q7UA20	Q7ua20 synechococc	766	6	1.6	102	2	Q8BFL8	Q8bfl8 uncultured
694	6	1.6	85	2	Q82QMB	Q82qm8 streptomyce	767	6	1.6	103	2	Q8SPV2	Q8spv2 skeletonema
695	6	1.6	85	2	Q9PBP3	Q9pbp3 xylella fas	768	6	1.6	103	2	Q8SPV3	Q8spv3 skeletonema
696	6	1.6	86	2	Q7CQEQ	Q7cqqo giardia lam	769	6	1.6	103	2	Q87672	Q87672 aeromonas h
697	6	1.6	86	2	Q9ZEM1	Q9zem1 lactobacill	770	6	1.6	103	2	Q8GAZ0	Q8gaz0 burkholderi
698	6	1.6	86	2	Q8FSL5	Q8fsl5 corynebacte	771	6	1.6	103	2	Q9D325	Q9d325 mus musculu
699	6	1.6	87	2	Q85JB4	Q85jb4 harpochytri	772	6	1.6	104	1	GAST_RAT	P04563 rattus norv
700	6	1.6	87	2	Q85MC3	Q85mc3 monoblephar	773	6	1.6	104	1	IAA_STRTE	P01092 streptomyce
701	6	1.6	87	2	Q85MD4	Q85md4 harpochytri	774	6	1.6	104	2	Q27339	Q27339 methanobact
702	6	1.6	87	2	Q7XQS3	Q7xqs3 oryza sativ	775	6	1.6	104	2	Q8L7N3	Q8l7n3 arabidopsis
703	6	1.6	87	2	Q93A12	Q93ai2 uncultured	776	6	1.6	104	2	Q65KV0	Q65kv0 bacillus li
704	6	1.6	89	2	Q7YTD7	Q7ytd7 heterodera	777	6	1.6	104	2	Q87A05	Q87a05 xylella fas
705	6	1.6	89	2	Q99593	Q99593 chalcides v	778	6	1.6	104	2	Q89G23	Q89g23 bradyrhizob
706	6	1.6	89	2	Q883J7	Q883j7 pseudomonas	779	6	1.6	104	2	Q9PA51	Q9pa51 xylella fas
707	6	1.6	89	2	Q6MCH6	Q6mch6 parachlamyd	780	6	1.6	105	1	RT02_SCHPO	Q42859 schizosacch
708	6	1.6	90	2	Q31729	Q31729 bacillus su	781	6	1.6	105	2	Q8U3G9	Q8u3g9 pyrococcus
709	6	1.6	91	2	Q99588	Q99588 chalcides s	782	6	1.6	105	2	Q9MF48	Q9mf48 beta vulgar
710	6	1.6	91	2	P94908	P94908 microbacter	783	6	1.6	105	2	Q6UTC8	Q6ut8 uncultured
711	6	1.6	91	2	Q6FDD4	Q6fdd4 acinetobact	784	6	1.6	106	2	Q7S3R0	Q7s3r0 neurospora
712	6	1.6	92	2	Q9HQM9	Q9hqm9 halobacteri	785	6	1.6	106	2	Q7PTU6	Q7ptu6 anopheles g
713	6	1.6	92	2	Q7ML36	Q7mla6 pseudomonas	786	6	1.6	106	2	Q9GS57	Q9gs57 xylocopa ol
714	6	1.6	92	2	Q7MPM9	Q7mpm9 vibrio vuln	787	6	1.6	106	2	Q7VIU6	Q7viu6 helicobacte
715	6	1.6	92	2	Q7MSS7	Q7ms7 wolinnella s	788	6	1.6	107	2	Q6B343	Q6b343 trypanosoma
716	6	1.6	93	2	Q6Z012	Q6z012 oryza sativ	789	6	1.6	107	2	Q6JSR7	Q6jsr7 craterostig
717	6	1.6	94	2	Q99585	Q99585 eumeces alg	790	6	1.6	107	2	Q53478	Q53478 mycobacteri
718	6	1.6	94	2	Q6LDL8	Q6ldl8 pseudomonas	791	6	1.6	107	2	Q92C18	Q92c18 listeria mo
719	6	1.6	94	2	Q8XGL8	Q8xgl8 salmonella	792	6	1.6	107	2	Q720K9	Q720k9 listeria mo
720	6	1.6	94	2	Q73TT9	Q73tt9 mycobacteri	793	6	1.6	107	2	Q7AF07	Q7ap07 listeria in
721	6	1.6	94	2	Q7CP79	Q7cpt9 salmonella	794	6	1.6	107	2	Q7VES9	Q7ves9 mycobacteri
722	6	1.6	95	2	Q99586	Q99586 chalcides m	795	6	1.6	107	2	Q994M2	Q994m2 human immun
723	6	1.6	95	2	Q7UPR3	Q7upe3 rhodopirell	796	6	1.6	107	2	Q6S846	Q6s846 human immun
724	6	1.6	95	2	Q7VI16	Q7vil6 helicobacte	797	6	1.6	107	2	Q6X6T8	Q6x6t8 human immun
725	6	1.6	96	2	Q7YV77	Q7yv77 trypanosoma	798	6	1.6	107	2	Q7SQ50	Q7sq50 human immun
726	6	1.6	96	2	Q7YVX8	Q7yvx8 trypanosoma	799	6	1.6	108	2	Q6H7A9	Q6h7a9 oryza sativ
727	6	1.6	97	2	Q68EA3	Q68ea3 homo sapien	800	6	1.6	108	2	Q87J57	Q87j57 vibrio para
728	6	1.6	97	2	Q7B154	Q7b154 streptomyce	801	6	1.6	108	2	Q9HVK7	Q9hvk7 pseudomonas
729	6	1.6	97	2	Q7UTP1	Q7utp1 rhodopirell	802	6	1.6	108	2	Q91OE8	Q91oe8 pseudomonas
730	6	1.6	97	2	Q9R3P2	Q9r3p2 streptomyce	803	6	1.6	108	2	Q80ZN3	Q80zn3 mus musculu
731	6	1.6	98	2	Q61KL3	Q6ikl3 drosophila	804	6	1.6	109	1	FEL2_FELCA	P30440 felis silve
732	6	1.6	98	2	Q9VB45	Q9vb45 drosophila	805	6	1.6	109	1	RNP2_ARCFU	Q29761 archaeoglob
733	6	1.6	98	2	Q8U551	Q8u551 agrobacteri	806	6	1.6	109	2	Q74120	Q74120 phycomyces
734	6	1.6	98	2	Q930V7	Q930v7 rhizobium m	807	6	1.6	109	2	Q7NLU3	Q7nlu3 gloeobacter
735	6	1.6	98	2	Q748N0	Q748n0 geobacter s	808	6	1.6	109	2	Q7TTC3	Q7ttc3 rhodopirell
736	6	1.6	99	2	Q98ND4	Q98nd4 rhizobium l	809	6	1.6	109	2	Q7USS0	Q7uss0 rhodopirell
737	6	1.6	99	2	Q6N3V3	Q6n3v3 rhodopseudo	810	6	1.6	109	2	Q6WJ07	Q6wj07 mus musculu
738	6	1.6	99	2	Q705D8	Q705d8 human papil	811	6	1.6	109	2	Q8C7P2	Q8c7p2 mus musculu
739	6	1.6	100	1	SECG_AQUAE	Q66505 aquifex aeo	812	6	1.6	110	2	Q96ZD1	Q96zd1 sulfolobus
740	6	1.6	100	2	Q8TM07	Q8tm07 methanosarc	813	6	1.6	110	2	Q6A8E3	Q6a8e3 propionibac
741	6	1.6	100	2	Q7Y8W3	Q7y8w3 portunus tr	814	6	1.6	110	2	Q73YI1	Q73yi1 mycobacteri
742	6	1.6	100	2	Q69XG5	Q69xg5 oryza sativ	815	6	1.6	110	2	Q74H31	Q74h31 geobacter s
743	6	1.6	100	2	Q06409	Q06409 mycobacteri	816	6	1.6	110	2	Q7VD16	Q7vd16 prochloroco
744	6	1.6	100	2	Q98DR6	Q98dk6 rhizobium l	817	6	1.6	110	2	Q823Z8	Q823z8 chlamydomphi
745	6	1.6	100	2	Q7U114	Q7ult4 mycobacteri	818	6	1.6	110	2	Q884F0	Q884f0 pseudomonas
746	6	1.6	100	2	Q8FV09	Q8fvq9 brucella su	819	6	1.6	111	2	Q8TQ56	Q8tq56 methanosarc
747	6	1.6	101	1	GAST_MOUSE	P48757 mus musculu	820	6	1.6	111	2	Q6SK48	Q6sk48 arthrobacte
748	6	1.6	101	2	Q9HI40	Q9hi40 thermoplasm	821	6	1.6	111	2	Q6DLB2	Q6dlb2 erwinia car
749	6	1.6	101	2	Q96NX0	Q96nx0 homo sapien	822	6	1.6	111	2	Q81LA7	Q81la7 rattus norv
750	6	1.6	101	2	Q69T44	Q69t44 oryza sativ	823	6	1.6	111	2	Q9WAY1	Q9way1 tt virus. o
751	6	1.6	101	2	P76933	P76933 escherichia	824	6	1.6	111	2	Q9WB07	Q9wb07 tt virus. o
752	6	1.6	101	2	Q92PJ2	Q92pj2 rhizobium m	825	6	1.6	112	2	Q8HIW2	Q8hiw2 phaseolus v
753	6	1.6	101	2	Q6A5U6	Q6a5u6 propionibac	826	6	1.6	112	2	Q82R15	Q82ri5 streptomyce
754	6	1.6	101	2	Q6LIR64	Q6lir64 photobacter	827	6	1.6	113	2	Q9Y9K8	Q9y9k8 aeropyrum p
755	6	1.6	101	2	Q880J0	Q880j0 pseudomonas	828	6	1.6	113	2	Q65CM3	Q65cm3 caenorhabdi
756	6	1.6	101	2	Q9CPR2	Q9cpr2 mus muscu	829	6	1.6	113	2	Q49878	Q49878 mycobacteri
757	6	1.6	102	2	Q8ZV70	Q8zvt0 pyrobaculum	830	6	1.6	114	1	IR03_HCMVA	F17142 human cytom
758	6	1.6	102	2	Q24939	Q24939 fasciola he	831	6	1.6	114	2	Q84T81	Q84t81 oryza sativ
759	6	1.6	102	2	Q94GT0	Q94gt0 oryza sativ	832	6	1.6	114	2	Q640X6	Q640x6 xenopus lae
760	6	1.6	102	2	Q7G7F0	Q7g7f0 oryza sativ	833	6	1.6	115	2	Q8SV99	Q8sv99 encephalito
761	6	1.6	102	2	Q6ZZU9	Q6zzu9 streptomyce	834	6	1.6	115	2	Q6EPD9	Q6epd9 oryza sativ

835	6	1.6	115	2	Q68JE0	Q68je0 escherichia	908	6	1.6	122	2	Q8JT33	Q8jt33 hepatitis e
836	6	1.6	115	2	Q83W90	Q83w90 escherichia	909	6	1.6	122	2	Q7ZJW8	Q7zjw8 human immun
837	6	1.6	115	2	Q9S117	Q9s117 escherichia	910	6	1.6	123	1	VST1_HEVBU	P29j25 hepatitis e
838	6	1.6	115	2	Q9S135	Q9s135 escherichia	911	6	1.6	123	1	VST1_HEVME	Q03499 hepatitis e
839	6	1.6	115	2	Q97RR3	Q97rr3 streptococc	912	6	1.6	123	1	VST1_HEVNY	Q04612 hepatitis e
840	6	1.6	115	2	Q8CZ01	Q8cz01 streptococc	913	6	1.6	123	1	Q8T8T7	Q8t8t7 drosophila
841	6	1.6	115	2	Q8FDS7	Q8fds7 escherichia	914	6	1.6	123	2	Q6UJ97	Q6uj97 ovis aries
842	6	1.6	115	2	Q6NVJ2	Q6nvj2 homo sapien	915	6	1.6	123	2	Q90299	Q90299 hepatitis e
843	6	1.6	116	2	Q6JSU5	Q6jsu5 strigamia b	916	6	1.6	123	2	Q91854	Q91854 hepatitis e
844	6	1.6	116	2	Q94N43	Q94n43 trachurus j	917	6	1.6	123	2	Q68984	Q68984 hepatitis e
845	6	1.6	116	2	Q6XFX3	Q6xfx3 nectarinia	918	6	1.6	123	2	Q59412	Q59412 hepatitis e
846	6	1.6	116	2	Q6XFX3	Q6xfx3 nectarinia	919	6	1.6	123	2	Q77X79	Q77x79 hepatitis e
847	6	1.6	116	2	Q8HK08	Q8hkt0 salarias fa	920	6	1.6	123	2	Q81877	Q81877 hepatitis e
848	6	1.6	116	2	Q8HL21	Q8hl21 carangoides	921	6	1.6	123	2	Q89803	Q89803 hepatitis e
849	6	1.6	116	2	Q8HM20	Q8hm20 caulophryne	922	6	1.6	123	2	Q9WLK2	Q9wlk2 hepatitis e
850	6	1.6	116	2	Q64053	Q64053 bacterioph	923	6	1.6	123	2	Q9YIA4	Q9yia4 cyprinus ca
851	6	1.6	116	2	Q62M00	Q62m00 burkholderi	924	6	1.6	123	2	Q8UEK9	Q8uek9 human immun
852	6	1.6	116	2	Q31967	Q31967 bacillus su	925	6	1.6	124	2	Q6X6J4	Q6x6j4 human immun
853	6	1.6	116	2	Q8Y8U3	Q8y8u3 listeria mo	926	6	1.6	124	2	Q8TRH5	Q8trh5 methanosarc
854	6	1.6	116	2	Q82RG7	Q82rg7 streptomyc	927	6	1.6	124	2	Q9GS49	Q9gs49 xylocopa fr
855	6	1.6	116	2	Q8CEH7	Q8ceh7 mus musculu	928	6	1.6	124	2	Q8XWZ6	Q8xwz6 ralestonia s
856	6	1.6	116	2	Q902P0	Q902p0 human immun	929	6	1.6	124	2	Q8XYS8	Q8xys8 ralestonia s
857	6	1.6	116	2	Q90ML6	Q90ml6 human immun	930	6	1.6	124	2	Q8XJL0	Q8xjl0 rhizobium l
858	6	1.6	116	2	Q6H1M5	Q6h1m5 human immun	931	6	1.6	125	2	Q8A0F3	Q8a0f3 panax gins
859	6	1.6	116	2	Q6H1Q2	Q6h1q2 human immun	932	6	1.6	125	2	Q8A0F3	Q8a0f3 bacteroides
860	6	1.6	116	2	Q6HLR1	Q6hlr1 human immun	933	6	1.6	125	2	Q9HJV8	Q9hvj8 pseudomonas
861	6	1.6	116	2	Q7ZMH7	Q7znh7 human immun	934	6	1.6	125	2	Q8QOB8	Q8qob8 equus cabal
862	6	1.6	116	2	Q8AD81	Q8ad81 human immun	935	6	1.6	126	2	Q8ZX16	Q8zx16 pyrobaculum
863	6	1.6	116	2	Q8AD97	Q8ad97 human immun	936	6	1.6	126	2	Q6CJM0	Q6cjm0 kluyveromyc
864	6	1.6	116	2	Q8ADN3	Q8adn3 human immun	937	6	1.6	126	2	Q86Y17	Q86yi17 homo sapien
865	6	1.6	116	2	Q8ADQ7	Q8adq7 human immun	938	6	1.6	126	2	Q9GS53	Q9gs53 xylocopa mi
866	6	1.6	116	2	Q8ADRS	Q8adr5 human immun	939	6	1.6	126	2	Q6R9H1	Q6r9h1 zea mays fm
867	6	1.6	116	2	Q8ADX9	Q8adx9 human immun	940	6	1.6	126	2	Q9TIF5	Q9tif5 lactobacill
868	6	1.6	116	2	Q8ADY7	Q8ady7 human immun	941	6	1.6	126	2	Q67U99	Q67u99 oryza sativ
869	6	1.6	116	2	Q8ADZ5	Q8adz5 human immun	942	6	1.6	126	2	Q9LUG3	Q9ljg3 chlorella v
870	6	1.6	116	2	Q8AE44	Q8ae44 human immun	943	6	1.6	127	2	Q8JBZ7	Q8jbz7 human immun
871	6	1.6	116	2	Q9QM85	Q9qm85 human immun	944	6	1.6	127	2	Q26450	Q26450 hirudo medi
872	6	1.6	117	2	Q69U63	Q69u63 oryza sativ	945	6	1.6	127	2	Q7WU43	Q7wu43 thermotoga
873	6	1.6	117	2	Q9RH52	Q9rh52 streptomyc	946	6	1.6	128	1	Y070_TREPA	Q83109 treponema p
874	6	1.6	117	2	Q8YFC5	Q8yfc5 brucella me	947	6	1.6	128	2	Q6ZB88	Q6zb88 oryza sativ
875	6	1.6	117	2	Q981N7	Q981n7 rhizobium l	948	6	1.6	128	2	Q72JA7	Q72ja7 thermus the
876	6	1.6	117	2	Q722B7	Q722b7 listeria mo	949	6	1.6	128	2	Q747B5	Q747b5 geobacter s
877	6	1.6	117	2	Q7WBP0	Q7wbp0 bordetella	950	6	1.6	128	2	Q89MH8	Q89mh8 bradyrhizob
878	6	1.6	117	2	Q6AY31	Q6ay31 rattus norv	951	6	1.6	129	1	FN14_MOUSE	Q9cr75 m tumor nec
879	6	1.6	117	2	Q9DAA3	Q9daa3 mus musculu	952	6	1.6	129	2	Q9UR42	Q9ur42 neurospora
880	6	1.6	118	1	VAG1_PANTR	Q862z6 pan troglod	953	6	1.6	129	2	Q9URP2	Q9urp2 neurospora
881	6	1.6	118	1	VAG2_HUMAN	Q95670 homo sapien	954	6	1.6	129	2	Q9URP3	Q9urp3 neurospora
882	6	1.6	118	1	VAG2_MOUSE	Q9wt44 mus musculu	955	6	1.6	129	2	Q7L690	Q7l690 homo sapien
883	6	1.6	118	1	VAG2_PIG	Q9tsv6 sus scrofa	956	6	1.6	129	2	Q26448	Q26448 hirudo medi
884	6	1.6	118	2	Q97CQ7	Q97cq7 thermoplasm	957	6	1.6	129	2	Q82448	Q82448 escherichia
885	6	1.6	118	2	Q9V479	Q9v479 drosophila	958	6	1.6	129	2	Q82903	Q82903 escherichia
886	6	1.6	118	2	Q88SP6	Q88sp6 lactobacill	959	6	1.6	129	2	Q7UZ89	Q7uz89 rhodopirell
887	6	1.6	118	2	Q8R2H0	Q8r2h0 rattus norv	960	6	1.6	129	2	Q88VV4	Q88vv4 lactobacill
888	6	1.6	118	2	Q8BKV3	Q8bkv3 mus musculu	961	6	1.6	129	2	Q88VRP6	Q88vrp6 bradyrhizob
889	6	1.6	119	2	Q8TQL3	Q8tdl3 methanosarc	962	6	1.6	129	2	Q9RC47	Q9rc47 bacillus ha
890	6	1.6	119	2	Q9CTI1	Q9cti1 mus musculu	963	6	1.6	129	2	Q6PBU7	Q6pbu7 brachydanio
891	6	1.6	119	2	Q7ZMI6	Q7zmi6 human immun	964	6	1.6	130	2	Q6BKW8	Q6bkw8 debaryomyc
892	6	1.6	120	2	Q7R9P6	Q7r9p6 plasmodium	965	6	1.6	130	2	Q6CQ54	Q6cq54 kluyveromyc
893	6	1.6	120	2	Q8RSB3	Q8rsb3 oryza sativ	966	6	1.6	130	2	Q9GS61	Q9gs61 xylocopa pu
894	6	1.6	120	2	Q7G670	Q7g670 oryza sativ	967	6	1.6	130	2	Q9SM56	Q9sm56 platyhamni
895	6	1.6	121	2	Q6F9K8	Q6fk8 acinetobact	968	6	1.6	130	2	Q8MT58	Q8mt58 rhizobium l
896	6	1.6	121	2	Q73JC5	Q73jc5 treponema d	969	6	1.6	130	2	Q98MT8	Q98mt8 rhizobium l
897	6	1.6	121	2	Q7UWG9	Q7uwg9 rhodopirell	970	6	1.6	130	2	Q73KP8	Q73kp8 treponema d
898	6	1.6	121	2	Q83LA3	Q83la3 shigella fl	971	6	1.6	130	2	Q746J0	Q746j0 thermus the
899	6	1.6	121	2	Q89U33	Q89u33 bradyrhizob	972	6	1.6	130	2	Q8FAB0	Q8fab0 escherichia
900	6	1.6	122	1	GLN2_METIV	P51604 methanobact	973	6	1.6	130	2	Q9A9A4	Q9a9a4 caulobacter
901	6	1.6	122	2	Q8T7G4	Q8tzg4 pyrococcus	974	6	1.6	130	2	Q8C4C8	Q8c4c8 mus musculu
902	6	1.6	122	2	Q9S7P8	Q9s7p8 arabidopsis	975	6	1.6	131	2	Q6BRG3	Q6brg3 debaryomyc
903	6	1.6	122	2	Q63S49	Q63s49 burkholderi	976	6	1.6	131	2	Q6ILG7	Q6ilg7 drosophila
904	6	1.6	122	2	Q7NKT6	Q7nkt6 gloeobacter	977	6	1.6	131	2	Q735X9	Q735x9 bacillus ce
905	6	1.6	122	2	Q88QP7	Q88qp7 pseudomonas	978	6	1.6	131	2	Q82QP5	Q82qp5 streptomyc
906	6	1.6	122	2	Q89T22	Q89t22 bradyrhizob	979	6	1.6	131	2	Q87UT1	Q87ut1 pseudomonas
907	6	1.6	122	2	Q8DJ06	Q8dj06 synecococc	980	6	1.6	131	2	Q9D2I8	Q9d2i8 mus musculu

DR Pfam: PF00781; DAGK cat; 1.
 DR ProDom: PD005043; DAGK; 1.
 DR SMART: SM00046; DAGK; 1.
 KW ATP-binding; Calmodulin-binding; Kinase; Transferase.
 FT CONFLICT 6 Missing (in Ref. 4).
 FT CONFLICT 11 NA -> KP (in Ref. 4).
 FT CONFLICT 114 115 V -> M (in Ref. 2).
 FT CONFLICT 251 251 V -> I (in Ref. 2).
 FT CONFLICT 260 260 L -> F (in Ref. 2).
 FT CONFLICT 302 302 L -> G (in Ref. 4).
 FT CONFLICT 325 325 V -> M (in Ref. 3).
 FT CONFLICT 337 337 V -> M (in Ref. 3).
 SQ SEQUENCE 384 AA; 42517 MW; EB04A7F2034C2DB0 CRC64;

Query Match 87.5%; Score 336; DB 1; Length 384;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPKRCVLLNPRGKGKALQLFSSHVQPLLAEEAIEISFTLMTERRNHA 60
 Db 1 MDPAGGPRGVLPKRCVLLNPRGKGKALQLFSSHVQPLLAEEAIEISFTLMTERRNHA 60

QY 61 RELVSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 Db 61 RELVSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

QY 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
 Db 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180

QY 181 SEKYRLGEMRFTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240
 Db 181 SEKYRLGEMRFTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240

QY 241 LEEPVPSHWTVVPDEDFVLVALLHSHLGSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
 Db 241 LEEPVPSHWTVVPDEDFVLVALLHSHLGSEMFAPMGRCAGVMHLFYVRAGVSRAML 300

QY 301 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPKDGKG 336
 Db 301 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPKDGKG 336

RESULT 2
 Q8N632 PRELIMINARY; PRT; 470 AA.
 AC Q8N632;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Sphingosine kinase 1.
 GN Name=SPHK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodríguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030553; AAH30553.1; -.
 DR EMBL; BC014439; AAH14439.1; -.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0005624; C:membrane fraction; ISS.
 DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
 DR GO; GO:0000287; F:magnesium ion binding; ISS.
 DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
 DR GO; GO:0046521; P:sphingoid catabolism; ISS.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR InterPro; IPR001206; DAGKc.
 DR Pfam; PF00781; DAGK_cat; 1.
 DR ProDom; PD005043; DAGK; 1.
 DR SMART; SM00046; DAGK; 1.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 KW Kinase.
 SQ SEQUENCE 470 AA; 51084 MW; 5172E93A38C7CC17 CRC64;

Query Match 87.5%; Score 336; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPKRCVLLNPRGKGKALQLFSSHVQPLLAEEAIEISFTLMTERRNHA 60
 Db 87 MDPAGGPRGVLPKRCVLLNPRGKGKALQLFSSHVQPLLAEEAIEISFTLMTERRNHA 146

QY 61 RELVSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 Db 147 RELVSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 206

QY 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
 Db 207 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 266

QY 181 SEKYRLGEMRFTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240
 Db 267 SEKYRLGEMRFTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 326

QY 241 LEEPVPSHWTVVPDEDFVLVALLHSHLGSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
 Db 327 LEEPVPSHWTVVPDEDFVLVALLHSHLGSEMFAPMGRCAGVMHLFYVRAGVSRAML 386

QY 301 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPKDGKG 336
 Db 387 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPKDGKG 422

RESULT 3
 Q96GK1 PRELIMINARY; PRT; 398 AA.
 AC Q96GK1;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Sphingosine kinase 1.
 GN Name=SPHK1;
 OS Homo sapiens (Human).


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RESULT 5
Q96HV8
ID Q96HV8 PRELIMINARY; PRT; 384 AA.
AC Q96HV8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SPHK1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TX TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Cren E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
TX TISSUE=Skin;
RX Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC008040; AAH08040.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE 3; UNKNOWN 1.
SQ SEQUENCE 384 AA; 42470 MW; F82995FF306113B0 CRC64;

Query Match 61.2%; Score 235; DB 2; Length 384;
Best Local Similarity 99.7%; Pred. No. 6e-226;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPAGGPRGVLPRPCRVLLNPRGGKALQQLFRSHVQPLLAEEISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKALQQLFRSHVQPLLAEEISFTMLTERRNHA 60

Qy 61 RELVSRSEELGRWDALVVMGDLHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVSRSEELGRWDALVVMGDLHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120

Qy 121 NHVAGYEQVTNEDLLTCTLLLCRLSLSPNNLLSLHTASGLRFLSVLSLAWGIADVDLE 180
Db 121 NHVAGYEQVTNEDLLTCTLLLCRLSLSPNNLLSLHTASGLRFLSVLSLAWGIADVDLE 180

RESULT 6
Q9NOA5
ID Q9NOA5 PRELIMINARY; PRT; 329 AA.
AC Q9NOA5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Unnamed protein product.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046025; BAB01607.1; -.
DR GO; GO:0005823; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE 3; UNKNOWN 1.
SQ SEQUENCE 329 AA; 36393 MW; 7F430ABD0CA5FDC7 CRC64;

Query Match 32.6%; Score 125; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.9e-116;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CRVLVLLNPRGGKALQQLFRSHVQPLLAEEISFTMLTERRNHAELVSRSEELGRWDA 74
Db 15 CRVLVLLNPRGGKALQQLFRSHVQPLLAEEISFTMLTERRNHAELVSRSEELGRWDA 74

Qy 75 LVVMSGDGLHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNVHAGYEQVTNEDL 134
Db 75 LVVMSGDGLHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNVHAGYEQVTNEDL 134

Qy 135 LTNCT 139
Db 135 LTNCT 139

RESULT 7
Q91ZN3
ID Q91ZN3 PRELIMINARY; PRT; 381 AA.
AC Q91ZN3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sphingosine kinase 1a.
OX Name=Sphk1;

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OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Thompson D., Pyne S.:
RL SUBMITTED (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF415213; AAL07499.1; -.
DR MGD; MGI:1316649; Sphk1.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
KW Kinase.
SQ SEQUENCE 381 AA; 42344 MW; 2F2C1F10D59EB129 CRC64;

Query Match 8.6%; Score 33; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 7.4e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 109
Db 76 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 108

RESULT 8
Q8CI15 PRELIMINARY; PRT; 382 AA.
AC Q8CI15;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Sphingosine kinase 1.
GN Name=Sphk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettunen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC037710; AAH37710.1; -.
DR MGD; MGI:1316649; Sphk1.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
KW Kinase.
SQ SEQUENCE 382 AA; 42443 MW; B791FAA58FCE3D29 CRC64;

Query Match 8.6%; Score 33; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 7.4e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 109
Db 77 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 109

RESULT 9
O88886 PRELIMINARY; PRT; 388 AA.
AC O88886;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Sphingosine kinase.
GN Name=Sphk1; Synonyms=SPHK1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98395082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722;
RA Kohama T., Olivera A., Edsall L., Nagiec M.M., Dickson R., Spiegel S.;
RT "Molecular cloning and functional characterization of murine
RT sphingosine kinase.";
RL J. Biol. Chem. 273:23722-23728 (1998).
DR EMBL; AF068749; AAC61698.1; -.
DR MGD; MGI:1316649; Sphk1.
DR GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
DR GO; GO:0007205; P:protein kinase C activation; IEA.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
KW Kinase.
SQ SEQUENCE 388 AA; 43254 MW; 01EB032322542CAD CRC64;

Query Match 8.6%; Score 33; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 7.5e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 109
Db 83 VMSGDGLMHVVNGLMERPDWETAIQKPLCSLP 115

RESULT 10
O88885 PRELIMINARY; PRT; 504 AA.
AC O88885;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Sphingosine kinase (Fragment).
GN Name=Sphk1; Synonyms=SPHK1a;
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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98395082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722;
 RA Kohama T., Olivera A., Edsall L., Nagiec M.M., Dickson R., Spiegel S.;
 RT "Molecular cloning and functional characterization of murine
 RL sphingosine kinase.";
 RL J. Biol. Chem. 273:23722-23728 (1998).
 DR EMBL; AF068748; AAC61697.1; -;
 DR MGDI; MGI:1316649; Spkl1.
 DR GO; GO:0004143; F-diacylglycerol kinase activity; IEA.
 DR GO; GO:0007205; P-protein kinase C activation; IEA.
 DR InterPro; IPR001206; DAGKC.
 DR Pfam; PF00781; DAGK cat; 1.
 DR ProDom; PD005043; DAGKC; 1.
 DR SMART; SM00046; DAGKC; 1.
 KW Kinase.
 FT NON_TER
 SQ SEQUENCE 504 AA; 55119 MW; 2AAFEBA72027F509 CRC64;
 Query Match 8.6%; Score 33; DB 2; Length 504;
 Best Local Similarity 100.0%; Pred. No. 9.3e-24;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 77 VMSGDGLMHEVNVGLMERPDWETAQKPLCSLP 109
 Db 199 VMSGDGLMHEVNVGLMERPDWETAQKPLCSLP 231
 RESULT 11
 Q91V26 PRELIMINARY; PRT; 383 AA.
 AC Q91V26;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Sphingosine kinase 1f (Sphingosine kinase 1a) (Sphingosine kinase 1c)
 DE (Sphingosine kinase 1d) (Sphingosine kinase 1e).
 GN Names=sphk1f; Synonyms=sphk1a, sphk1c, sphk1d, sphk1e;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inamura T., Ohgane J., Ito S., Ogawa T., Hattori N., Tanaka S.,
 RA Shiota K.;
 RT "CpG island of rat sphingosine kinase-1 gene: tissue-dependent DNA
 RT methylation status and multiple alternative first exons.";
 RL Genomics 78:117-125 (2001).
 DR EMBL; AB049575; BAB62324.1; -;
 DR EMBL; AB049571; BAB62320.1; -;
 DR EMBL; AB049572; BAB62321.1; -;
 DR EMBL; AB049573; BAB62322.1; -;
 DR EMBL; AB049574; BAB62323.1; -;
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0005624; C:membrane fraction; ISS.
 DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
 DR GO; GO:000287; F:magnesium ion binding; ISS.
 DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
 DR GO; GO:0046521; P:sphingoid catabolism; ISS.
 DR Pfam; PF00781; DAGK cat; 1.
 DR ProDom; PD005043; DAGKC; 1.
 DR SMART; SM00046; DAGKC; 1.
 KW Kinase.
 SQ SEQUENCE 383 AA; 42418 MW; CAAD5817BF4B9507 CRC64;
 Query Match 5.7%; Score 22; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 7.5e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 VMSGDGLMHEVNVGLMERPDWE 98
 Db 77 VMSGDGLMHEVNVGLMERPDWE 98

RESULT 12
 Q642F6 PRELIMINARY; PRT; 383 AA.
 ID Q642F6;
 AC Q642F6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Sphingosine kinase 1.
 DE Name=Spkl1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC081738; AAH81738.1; -;
 KW Kinase.
 SQ SEQUENCE 383 AA; 42432 MW; 70B6E217AF812F77 CRC64;
 Query Match 5.7%; Score 22; DB 2; Length 383;
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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 77 VMSGDGLMHEVNVGLMERPDWE 98
 Db 77 VMSGDGLMHEVNVGLMERPDWE 98
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 ID Q8Y1S2;
 AC Q8Y1S2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE PROBABLE SIGNAL PEPTIDE PROTEIN
 GN Name=RS01518; OrderedLocNames=RSC0617;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.

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OX NCBI_TaxID=305;
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RP SEQUENCE FROM N.A.
RC STRAIN=GM1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002);
DR EMBL; AL646060; CAD14147.1; -.
KW Complete proteome.
SQ SEQUENCE 118 AA; 12054 MW; 955D9DEA2C16CF42 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 AGSGNALAA 28

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ90120.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki M.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074601; BAC11085.1; -.
SQ SEQUENCE 244 AA; 24989 MW; F11285DC202EFC43 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 LRLFLAME 307
Db 170 LRLFLAME 178

RESULT 15
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ID SPH2 HUMAN STANDARD; PRT; 654 AA.
AC Q9NR80; Q9BRN1; Q9HQ02; Q9NWU7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sphingosine kinase 2 (EC 2.7.1.-) (SK 2) (SPK 2).
CN Name=SPK2;
OS Homo sapiens (Human).
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION
RX MEDLINE=20347850; PubMed=10751414; DOI=10.1074/jbc.M002759200;
RA Liu H., Sugiyama M., Nava V.E., Edsall L.C., Kono K., Poulton S.,
RA Milstien S., Kohama T., Spiegel S.;
RT "Molecular cloning and functional characterization of a novel
RL J. Biol. Chem. 275:19513-19520(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.,
RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RL analysis of 500 novel complete protein coding human cDNAs.";
RN Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Eye, and Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.";
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-354 FROM N.A. (ISOFORM 3).
RC TISSUE=Carcinoma;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotohata T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 12:12:19 ; Search time 41 Seconds
(without alignments)
901.152 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 384
Sequence: 1 MDPAGPRGVLPKPCRLVL.....CVERPPSKPQQMPPPERPL 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	8	2.1	208	2 H83627	hypothetical prote
2	8	2.1	309	2 H69995	hypothetical prote
3	8	2.1	558	2 A33616	heterogeneous ribo
4	8	2.1	812	2 T34180	hypothetical prote
5	8	2.1	1088	2 B34106	protein kinase (EC
6	7	1.8	62	2 C64331	ribosomal protein
7	7	1.8	87	2 AF3030	hypothetical prote
8	7	1.8	89	2 T27015	hypothetical prote
9	7	1.8	97	2 H98254	IgE chain C3 regio
10	7	1.8	107	2 I68726	IgE chain C3 regio
11	7	1.8	107	2 I68730	hypothetical prote
12	7	1.8	119	2 S50770	hypothetical prote
13	7	1.8	128	2 G75308	histone H2A - Tryp
14	7	1.8	135	2 S25119	lamprin 2 precurs
15	7	1.8	139	1 C45051	transcription regu
16	7	1.8	185	2 A95086	conserved hypotet
17	7	1.8	185	2 E97953	probable transcript
18	7	1.8	193	2 H83356	hypothetical prote
19	7	1.8	212	2 S76486	probable transaldo
20	7	1.8	221	2 AC0272	probable regulator
21	7	1.8	221	2 H70981	probable TetR-fam
22	7	1.8	223	2 F86998	hypothetical prote
23	7	1.8	238	2 S41313	probable polyprote
24	7	1.8	239	2 D85073	phosphoribosylform
25	7	1.8	245	2 A83003	conserved hypotet
26	7	1.8	257	2 C83005	glycosyltransferas
27	7	1.8	268	2 B97189	exopolysaccharide
28	7	1.8	278	2 D70036	ribosomal protein
29	7	1.8	285	2 S52681	

30	7	1.8	292	2 T36914	probable integral
31	7	1.8	305	2 T20470	hypothetical prote
32	7	1.8	306	2 AE1394	conserved hypotet
33	7	1.8	306	2 AH1769	conserved hypotet
34	7	1.8	313	2 T35935	transcription regu
35	7	1.8	334	2 A72217	Holliday junction
36	7	1.8	338	2 D87801	protein ClOGli.7 (
37	7	1.8	352	2 T35031	probable transcrip
38	7	1.8	352	2 T05418	hypothetical prote
39	7	1.8	358	2 F70583	hypothetical prote
40	7	1.8	369	2 B81039	riboflavin-specifi
41	7	1.8	382	2 T35709	hypothetical prote
42	7	1.8	385	2 G82789	permease XF0589 li
43	7	1.8	388	1 EHMS	Ig epsilon chain C
44	7	1.8	399	2 E83030	nicotinate phospho
45	7	1.8	400	2 T35334	probable membrane
46	7	1.8	402	2 F72340	probable carboxyl-
47	7	1.8	423	1 EHMS	Ig epsilon chain C
48	7	1.8	426	2 T50715	amidase regulator
49	7	1.8	428	2 A35534	tetrahydrofolylpol
50	7	1.8	440	2 D82100	mesj protein VC224
51	7	1.8	449	2 C83634	hypothetical prote
52	7	1.8	453	2 D90433	conserved hypotet
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54	7	1.8	457	2 T25612	hypothetical prote
55	7	1.8	459	2 A99932	hypothetical prote
56	7	1.8	472	2 F69658	hypothetical prote
57	7	1.8	476	2 T30781	kelch protein homo
58	7	1.8	492	2 C84142	hypothetical prote
59	7	1.8	496	2 S46459	glycine receptor b
60	7	1.8	496	2 JH0165	glycine receptor b
61	7	1.8	497	2 G02031	glycine receptor b
62	7	1.8	508	1 UFBSHS	histidine ammonia-
63	7	1.8	508	2 S75478	leucine aminopepti
64	7	1.8	518	2 T13652	hypothetical prote
65	7	1.8	527	2 E87610	alkyl hydroperoxid
66	7	1.8	548	2 S38864	Ig epsilon chain C
67	7	1.8	552	2 A12256	hypothetical prote
68	7	1.8	571	2 AC1216	ABC transporters,
69	7	1.8	571	2 AH1569	ABC transporters,
70	7	1.8	574	2 T39829	amino-acid permeas
71	7	1.8	586	2 B90659	Rhs core protein l
72	7	1.8	586	2 H85509	hypothetical prote
73	7	1.8	636	2 I61718	neu differentiation
74	7	1.8	639	2 I61719	neu differentiation
75	7	1.8	645	2 A12463	DNA gyrase B chain
76	7	1.8	662	2 I61722	neu differentiation
77	7	1.8	683	2 S34961	synaptic vesicle p
78	7	1.8	694	2 D84811	hypothetical prote
79	7	1.8	760	1 C2MS	classical-compleme
80	7	1.8	809	2 F87458	conserved hypotet
81	7	1.8	815	2 T15402	hypothetical prote
82	7	1.8	882	2 G70781	hypothetical prote
83	7	1.8	901	2 A82290	cyanophycin synthe
84	7	1.8	930	2 B84505	probable retroelem
85	7	1.8	948	2 C82077	glutamate-ammonia-
86	7	1.8	955	2 A84553	probable mitotic c
87	7	1.8	996	2 G87687	hypothetical prote
88	7	1.8	1029	2 T30351	mucin-like protein
89	7	1.8	1196	2 T00715	hypothetical prote
90	7	1.8	1239	2 G86218	protein F22013.10
91	7	1.8	1253	2 S46948	arylphorin recepto
92	7	1.8	1253	2 S46949	arylphorin recepto
93	7	1.8	1268	2 B36502	insulin receptor-r
94	7	1.8	1306	2 A13592	insulin receptor-r
95	7	1.8	1306	2 T13592	hypothetical prote
96	7	1.8	1333	2 A37488	Ras guanine nucleo
97	7	1.8	1336	2 S25716	Ras guanine nucleo
98	7	1.8	1357	2 S57052	hypothetical prote
99	7	1.8	1390	2 A45455	nucleoporin 155 -
100	7	1.8	1481	1 QZDOP3	pyrimidine synthe
101	7	1.8	1513	2 T44045	hypothetical prote
102	7	1.8	1549	2 T13940	ankyrin - fruit fl

103	7	1.8	1952	2	T48814	hypotheical prote	176	6	1.6	134	2	S70811	hypotheical prote
104	6	1.6	19	2	B60822	cytochrome P450 UT	177	6	1.6	134	2	D84672	hypotheical prote
105	6	1.6	34	2	S56746	alpha-synuclein, N	178	6	1.6	135	2	AG1035	probable phage tai
106	6	1.6	38	2	B48147	tropomin I (altern	179	6	1.6	135	2	AF1740	hypotheical prote
107	6	1.6	41	1	B40236	structural protein	180	6	1.6	135	2	AB1370	hypotheical prote
108	6	1.6	41	2	T03926	nascent polypeptid	181	6	1.6	136	2	B81388	hypotheical prote
109	6	1.6	52	2	G83356	hypotheical prote	182	6	1.6	138	2	P65140	hypotheical prote
110	6	1.6	60	2	T34737	probable gas vesic	183	6	1.6	138	2	D90672	hypotheical prote
111	6	1.6	69	2	G69004	ferredoxin 2-oxogl	184	6	1.6	138	2	H85522	hypotheical prote
112	6	1.6	70	2	T06922	photosystem I chai	185	6	1.6	139	2	S77060	transposase sl1066
113	6	1.6	71	2	B89990	hypotheical prote	186	6	1.6	139	2	B69953	hypotheical prote
114	6	1.6	73	2	T20911	hypotheical prote	187	6	1.6	139	2	T49650	hypotheical prote
115	6	1.6	74	2	B40020	collagen alpha 1(X	188	6	1.6	139	2	T39660	modification methy
116	6	1.6	74	2	S75123	hypotheical prote	189	6	1.6	139	2	T46457	hypotheical prote
117	6	1.6	77	2	F69219	conserved hypothe	190	6	1.6	139	2	D95896	conserved hypothe
118	6	1.6	77	2	T06954	hypotheical prote	191	6	1.6	140	2	T29662	hypotheical prote
119	6	1.6	79	1	BVECCF	sopC protein - Esc	192	6	1.6	140	2	D72322	conserved hypothe
120	6	1.6	79	2	B89761	hypotheical prote	193	6	1.6	140	2	G87183	thioredoxin import
121	6	1.6	80	2	A48284	intestinal trefoil	194	6	1.6	140	2	H70809	probable thiX prot
122	6	1.6	80	2	C95994	hypotheical prote	195	6	1.6	141	2	G87682	hypotheical prote
123	6	1.6	81	2	D95014	competence-induced	196	6	1.6	142	2	A95132	hypotheical prote
124	6	1.6	82	2	C75296	transcription regu	197	6	1.6	142	2	AB1635	hypotheical prote
125	6	1.6	83	2	T17809	hypotheical prote	198	6	1.6	143	2	S13238	tail fiber assembl
126	6	1.6	85	2	F82600	hypotheical prote	199	6	1.6	143	2	H81035	conserved hypothe
127	6	1.6	90	1	G69876	conserved hypothe	200	6	1.6	143	2	D81981	probable integral
128	6	1.6	90	2	T44137	hypotheical prote	201	6	1.6	144	2	S01898	psiB protein - Esc
129	6	1.6	91	2	T45132	hypotheical prote	202	6	1.6	144	2	S01897	psiB protein - Esc
130	6	1.6	92	2	H84264	hypotheical prote	203	6	1.6	144	2	T16824	hypotheical prote
131	6	1.6	92	2	S41662	L-phenylalanine ox	204	6	1.6	145	2	A75003	purine-binding che
132	6	1.6	92	2	A56413	major allergen Fel	205	6	1.6	145	2	T42187	psiB protein - Esc
133	6	1.6	94	2	A11057	conserved hypothe	206	6	1.6	145	2	A71160	probable purine-bi
134	6	1.6	98	2	G95272	hypotheical prote	207	6	1.6	146	2	S59575	probable membrane
135	6	1.6	98	2	A97632	hypotheical prote	208	6	1.6	147	2	AH2801	mutr like protein
136	6	1.6	100	1	F70309	protein export mem	209	6	1.6	147	2	B97581	hypotheical prote
137	6	1.6	100	2	B70547	hypotheical prote	210	6	1.6	148	2	S40148	integrin alpha-7A
138	6	1.6	101	2	S68861	gastrin precursor	211	6	1.6	150	2	S49617	cycl protein - Rhi
139	6	1.6	102	2	B66976	PG-family protein	212	6	1.6	150	2	JQ1183	histone H2A - gard
140	6	1.6	104	1	WISMAT	alpha-amylase inhi	213	6	1.6	150	2	T05295	hypotheical prote
141	6	1.6	104	2	H82527	conserved hypothe	214	6	1.6	151	2	C82982	deoxyuridine 5'-tr
142	6	1.6	104	2	A40910	gastrin precursor	215	6	1.6	151	2	G64497	hypotheical prote
143	6	1.6	104	2	A69037	conserved hypothe	216	6	1.6	151	2	PC4164	flagellar protein
144	6	1.6	105	2	T38300	ribosomal protein	217	6	1.6	151	2	G84131	hypotheical prote
145	6	1.6	105	2	S50352	hypotheical prote	218	6	1.6	152	2	G75184	probable transcrip
146	6	1.6	107	2	AU1227	hypotheical prote	219	6	1.6	152	2	T41998	hypotheical prote
147	6	1.6	107	2	AU1580	hypotheical prote	220	6	1.6	153	2	T09832	water-stress-induc
148	6	1.6	107	2	A70943	major allergen cha	221	6	1.6	153	2	T07772	disease resistance
149	6	1.6	107	2	A70943	probable repressor	222	6	1.6	154	2	F69477	NADH2 dehydrogenas
150	6	1.6	108	2	F83309	probable thioredox	223	6	1.6	155	2	T05169	Lsd1 protein homol
151	6	1.6	108	2	S40149	integrin alpha-7C	224	6	1.6	155	2	S48475	hypotheical prote
152	6	1.6	108	2	G83073	hypotheical prote	225	6	1.6	156	2	B64520	riboflavin synthas
153	6	1.6	109	2	C56413	major allergen Fel	226	6	1.6	156	2	G64856	probable membrane
154	6	1.6	113	2	F73006	hypotheical prote	227	6	1.6	156	2	AC1570	hypotheical prote
155	6	1.6	113	2	D72454	hypotheical prote	228	6	1.6	157	2	S12163	type II site-speci
156	6	1.6	114	2	S09752	hypotheical prote	229	6	1.6	157	2	T48683	hypotheical prote
157	6	1.6	115	2	G95084	conserved domain p	230	6	1.6	158	2	B96496	unknown protein, 5
158	6	1.6	115	2	C97952	hypotheical prote	231	6	1.6	158	2	S77127	hypotheical prote
159	6	1.6	116	2	T12804	hypotheical prote	232	6	1.6	160	2	A41144	growth arrest-rela
160	6	1.6	116	2	AH1174	B. subtilis YqkB p	233	6	1.6	160	2	T45309	small protein B [i
161	6	1.6	117	2	S20469	ERV1 protein - yea	234	6	1.6	160	2	H86978	6,7-dimethyl-8-rib
162	6	1.6	117	2	AG3451	murein hydrolase e	235	6	1.6	160	2	F86848	hypotheical prote
163	6	1.6	123	1	C44212	structural protein	236	6	1.6	161	2	B86284	Ti5D22.10 protein
164	6	1.6	123	1	VFWWE	structural protein	237	6	1.6	164	2	AD3478	hypotheical prote
165	6	1.6	125	2	F83072	hypotheical prote	238	6	1.6	166	2	A42524	A-ORF-E protein -
166	6	1.6	128	2	F71371	hypotheical prote	239	6	1.6	167	2	S60876	phosphorylation-ac
167	6	1.6	129	2	I61187	alpha-7A integrin	240	6	1.6	167	2	AH1106	hypotheical prote
168	6	1.6	129	2	JC5902	ubiquinol oxidase	241	6	1.6	169	2	A83134	conserved hypothe
169	6	1.6	129	2	T00282	hypotheical prote	242	6	1.6	170	2	AF1572	diol dehydrase (di
170	6	1.6	129	2	T44494	hypotheical prote	243	6	1.6	170	2	B55663	oligodendrocyte-sp
171	6	1.6	130	2	F87384	cytochrome c famil	244	6	1.6	171	2	G84421	probable auxin-ind
172	6	1.6	132	1	A69311	conserved hypothe	245	6	1.6	172	2	F83071	probable transcrip
173	6	1.6	132	2	S22303	histone H2A - Leis	246	6	1.6	173	2	T47279	hypotheical prote
174	6	1.6	132	2	S22391	histone H2A - Leis	247	6	1.6	173	2	D83168	heat shock protein
175	6	1.6	132	2	T25694	hypotheical prote	248	6	1.6	173	2	T22350	hypotheical prote

249	6	1.6	173	2	A95864	hypothetical prote	322	6	1.6	213	2	D90878	hypothetical prote
250	6	1.6	173	2	C97330	transcription regu	323	6	1.6	213	2	B90898	hypothetical prote
251	6	1.6	175	2	B95412	hypothetical prote	324	6	1.6	213	2	D86170	hypothetical prote
252	6	1.6	176	2	A86815	transcription regu	325	6	1.6	213	2	E85719	hypothetical prote
253	6	1.6	178	2	T33440	hypothetical prote	326	6	1.6	213	2	B85740	unknown protein en
254	6	1.6	178	2	H83061	hypothetical prote	327	6	1.6	214	2	A82195	serine esterase li
255	6	1.6	179	2	T42293	hypothetical prote	328	6	1.6	214	2	T34856	hypothetical prote
256	6	1.6	180	2	T18161	hypothetical prote	329	6	1.6	215	2	S29595	calmodulin-related
257	6	1.6	180	2	S06616	chorion protein s1	330	6	1.6	216	2	D72587	phosphoesterase-re
258	6	1.6	181	2	S69721	probable adenine p	331	6	1.6	216	2	S39625	EagI protein - Ent
259	6	1.6	181	2	E82333	oligoribonuclease	332	6	1.6	216	2	S35945	EagI protein - Ent
260	6	1.6	183	2	S03180	transforming prote	333	6	1.6	216	2	A10120	N-acylhomoserine l
261	6	1.6	183	2	G84609	hypothetical prote	334	6	1.6	216	2	S55682	ornithine decarbox
262	6	1.6	183	2	E83410	probable transcrip	335	6	1.6	216	2	C91047	hydrogenase-4 comp
263	6	1.6	184	1	D70177	4-methyl-5(b-hydro	336	6	1.6	216	2	C91047	hydrogenase-4 comp
264	6	1.6	184	2	AD1977	hypothetical prote	337	6	1.6	216	2	G85891	conserved hypothet
265	6	1.6	185	2	H82227	CDP-diacylglycerol	338	6	1.6	216	2	A72345	calmodulin-like pr
266	6	1.6	185	2	S64035	hypothetical prote	339	6	1.6	216	2	D84841	hypothetical prote
267	6	1.6	185	2	A72528	hypothetical prote	340	6	1.6	217	2	AB3476	H ₂ -transporting tw
268	6	1.6	187	2	F69583	alkyl hydroperoxid	341	6	1.6	219	2	S60641	hypothetical prote
269	6	1.6	187	2	G83815	hypothetical prote	342	6	1.6	220	2	B71811	hypothetical prote
270	6	1.6	188	2	A75382	hypothetical prote	343	6	1.6	220	2	UC7885	low-molecular-mass
271	6	1.6	189	2	T41472	60S ribosomal prot	344	6	1.6	221	2	E84227	hypothetical prote
272	6	1.6	189	2	S30172	mercury-binding pr	345	6	1.6	221	2	D86472	hypothetical prote
273	6	1.6	189	2	D71421	hypothetical prote	346	6	1.6	221	2	AE2055	hypothetical prote
274	6	1.6	190	2	T07720	VP829-like phospho	347	6	1.6	222	2	T36465	hypothetical prote
275	6	1.6	191	2	C87438	hypothetical prote	348	6	1.6	222	2	T19190	hypothetical prote
276	6	1.6	192	2	T46696	hypothetical prote	349	6	1.6	224	2	B27451	cutinase (EC 3.1.-
277	6	1.6	193	2	AH3639	cytochrome b561 li	350	6	1.6	224	2	T11354	H ₂ -transporting tw
278	6	1.6	193	2	AE2606	transcription regu	351	6	1.6	224	2	A26569	exotoxin A regulat
279	6	1.6	194	2	E84097	imidazoleglycerol-	352	6	1.6	225	2	B91104	probable ABC trans
280	6	1.6	194	2	B75613	conserved hypothet	353	6	1.6	225	2	E85949	probable ABC trans
281	6	1.6	194	2	D95924	transcription regu	354	6	1.6	225	2	S67772	hypothetical prote
282	6	1.6	196	2	S74510	signal peptidase I	355	6	1.6	225	2	D86370	26.4K hypothetical
283	6	1.6	196	2	T36667	probable small sec	356	6	1.6	225	2	C71289	hypothetical prote
284	6	1.6	196	2	S54050	hypothetical prote	357	6	1.6	226	2	PC6047	probable ABC-type
285	6	1.6	198	2	AF0968	hypothetical prote	358	6	1.6	226	2	F25973	pertussis toxin ch
286	6	1.6	198	2	E75599	conserved hypothet	359	6	1.6	227	1	WB8R31	chby protein - Rho
287	6	1.6	199	2	T36622	hypothetical prote	360	6	1.6	227	1	T10510	hypothetical prote
288	6	1.6	200	2	D70039	two-component resp	361	6	1.6	227	2	T75530	conserved hypothet
289	6	1.6	200	2	T29807	hypothetical prote	362	6	1.6	227	2	B69503	probable transcrip
290	6	1.6	201	2	F90253	hypothetical prote	363	6	1.6	228	2	T35418	ElB 19K/Bcl-2-inte
291	6	1.6	201	2	A64737	formate hydrogenly	364	6	1.6	228	2	I38863	SEB4D protein - hu
292	6	1.6	201	2	T44489	yadL protein - Esc	365	6	1.6	228	2	S38382	cytidylate kinase
293	6	1.6	201	2	A83599	hypothetical prote	366	6	1.6	228	2	C92141	hypothetical prote
294	6	1.6	201	2	AG0442	probable phosphosu	367	6	1.6	229	2	T39153	B-cell-specific me
295	6	1.6	203	2	B75303	conserved hypothet	368	6	1.6	229	2	A46527	SEB4B protein - hu
296	6	1.6	203	2	T36240	hypothetical prote	369	6	1.6	229	2	S38383	CpsC protein - Str
297	6	1.6	204	2	H70609	probable dna-3-met	370	6	1.6	230	2	JC5724	hypothetical prote
298	6	1.6	204	2	E91271	hypothetical prote	371	6	1.6	231	2	S76456	superoxide dismuta
299	6	1.6	204	2	E86112	hypothetical prote	372	6	1.6	231	2	AB3138	superoxide dismuta
300	6	1.6	204	2	S56390	hypothetical 23.5K	373	6	1.6	232	2	B98150	orotidine-5'-phosp
301	6	1.6	204	2	F87295	conserved hypothet	374	6	1.6	232	2	S43188	orotidine 5'-phosp
302	6	1.6	204	2	D97388	probable DNA-bind	375	6	1.6	232	2	B83285	conserved hypothet
303	6	1.6	205	2	S06867	crystallin (clone	376	6	1.6	232	2	C72105	disulfide bond cha
304	6	1.6	205	2	S49375	hemM protein - Pse	377	6	1.6	233	2	D86519	proline-rich prote
305	6	1.6	205	2	E83063	probable lipoprote	378	6	1.6	233	2	T36385	hypothetical prote
306	6	1.6	205	2	T33826	hypothetical prote	379	6	1.6	233	2	T47136	hypothetical prote
307	6	1.6	208	2	D83241	probable nuclease	380	6	1.6	234	1	S40854	hypothetical prote
308	6	1.6	208	2	AG1373	B. subtilis YnfK p	381	6	1.6	234	2	D86080	hypothetical prote
309	6	1.6	209	2	AE1743	preprotein translo	382	6	1.6	234	2	D91233	hypothetical prote
310	6	1.6	209	2	E82241	hypothetical prote	383	6	1.6	234	2	AB1078	phosphoheptose iso
311	6	1.6	209	2	D83879	hypothetical prote	384	6	1.6	234	2	AB1078	phosphoheptose iso
312	6	1.6	210	2	JS0180	scmatotropin precu	385	6	1.6	234	2	T35448	probable cytochrom
313	6	1.6	210	2	A57337	esal protein - Erw	386	6	1.6	234	2	B72671	hypothetical prote
314	6	1.6	210	2	C87305	hypothetical prote	387	6	1.6	235	2	G72501	hypothetical prote
315	6	1.6	210	2	F69983	hypothetical prote	388	6	1.6	236	2	T50908	hypothetical prote
316	6	1.6	211	2	A12616	GRPE protein limpo	389	6	1.6	237	1	A70522	hypothetical prote
317	6	1.6	211	2	A97399	grpe protein (hsp-	390	6	1.6	237	1	S74682	spore germination
318	6	1.6	212	2	D82546	conserved hypothet	391	6	1.6	238	2	T04166	hypothetical prote
319	6	1.6	212	2	AC3048	dethiobiotin synth	392	6	1.6	238	2	S76936	chaumatin-like pro
320	6	1.6	212	2	H98237	biod protein (Af31	393	6	1.6	238	2	AF1298	hypothetical prote
321	6	1.6	213	1	XUZM1	glutathione transf	394	6	1.6	238	2	AF1298	hypothetical prote

395	6	1.6	239	2	E84323	50S ribosomal prot	468	6	1.6	266	2	B95170	amino acid ABC tra
396	6	1.6	239	2	C72771	hypothetical prote	469	6	1.6	266	2	B98036	hypothetical prote
397	6	1.6	239	2	C83637	probable Atp-Bindi	470	6	1.6	266	2	AB1149	transport proteins
398	6	1.6	239	2	T42364	conserved hypotet	471	6	1.6	266	2	AB1508	transport proteins
399	6	1.6	240	2	AH0749	cell-division regu	472	6	1.6	267	1	DCUMOP	orotidine-5'-phosp
400	6	1.6	240	2	G83271	probable phosphodi	473	6	1.6	267	1	A90252	sugar ABC transpor
401	6	1.6	240	2	A95952	probable 2-deoxyl	474	6	1.6	267	2	B70487	thiamin biosynthes
402	6	1.6	241	1	R7HS5	ribosomal protein	475	6	1.6	267	2	B87648	phosphomethylprim
403	6	1.6	242	2	F83316	H+-transporting tw	476	6	1.6	267	2	B87665	hypothetical prote
404	6	1.6	242	2	T32122	hypothetical prote	477	6	1.6	268	2	H91087	probable enzyme [i
405	6	1.6	242	2	A11883	hypothetical prote	478	6	1.6	268	2	D71325	conserved hypotet
406	6	1.6	243	2	F83838	oxidoreductase (sh	479	6	1.6	268	2	B85933	probable enzyme yg
407	6	1.6	243	2	C95266	probable ABC trans	480	6	1.6	268	2	H65063	hypothetical prote
408	6	1.6	244	2	D75505	hypothetical prote	481	6	1.6	269	2	H82322	probable bis(5',nu
409	6	1.6	245	2	G64210	uracil DNA glycosy	482	6	1.6	269	2	A99396	conserved hypotet
410	6	1.6	245	2	A13485	hypothetical prote	483	6	1.6	270	2	B83784	hypothetical prote
411	6	1.6	246	2	A99426	enoyl CoA hydratase	484	6	1.6	271	2	AE2383	hypothetical prote
412	6	1.6	246	2	AG3644	flagellar biosynth	485	6	1.6	273	1	MMAGCG	membrane protein 1
413	6	1.6	246	2	A90165	conserved hypotet	486	6	1.6	273	2	A70585	hypothetical prote
414	6	1.6	246	2	C98774	hypothetical prote	487	6	1.6	274	2	T33371	hypothetical prote
415	6	1.6	247	1	A54662	myelin P0 protein	488	6	1.6	275	2	G98194	sugar ABC transpor
416	6	1.6	247	1	A53379	translation initia	489	6	1.6	275	2	AC3092	hypothetical prote
417	6	1.6	247	1	AH2848	conserved hypotet	490	6	1.6	275	2	B81022	VacJ-related prote
418	6	1.6	249	2	H83826	mannose-1-phosphat	491	6	1.6	276	2	S76992	probable bromide p
419	6	1.6	249	2	S03173	exotoxin A regulat	492	6	1.6	276	2	A72276	phosphate ABC tran
420	6	1.6	249	2	A10350	probable fibrial	493	6	1.6	276	2	T36288	probable ABC-type
421	6	1.6	250	2	AE1528	hypothetical prote	494	6	1.6	277	2	E98328	hypothetical prote
422	6	1.6	250	2	H83213	hypothetical prote	495	6	1.6	277	2	S63616	malG protein homol
423	6	1.6	251	2	F82977	transcription regu	496	6	1.6	277	2	S57381	protein disulfide
424	6	1.6	251	2	AH3533	spermidine/putresc	497	6	1.6	279	2	G75185	nicotinate-nucleot
425	6	1.6	251	2	S41587	hemD protein - Pse	498	6	1.6	279	2	A87360	hypothetical prote
426	6	1.6	251	2	A82989	uroporphyrinogen-I	499	6	1.6	279	2	G81966	probable periplasm
427	6	1.6	251	2	A83132	hypothetical prote	500	6	1.6	280	2	A70956	dihydroperate sy
428	6	1.6	251	2	A83660	hypothetical prote	501	6	1.6	280	2	S46699	hypothetical prote
429	6	1.6	251	2	B84016	hypothetical prote	502	6	1.6	280	2	H72504	hypothetical prote
430	6	1.6	252	2	A87124	probable enoyl-CoA	503	6	1.6	280	2	C30589	hypothetical prote
431	6	1.6	252	2	A32489	oncostatin M precu	504	6	1.6	281	2	C97155	spo0A protein, (Ch
432	6	1.6	252	2	D87397	hypothetical prote	505	6	1.6	281	2	D72351	hypothetical prote
433	6	1.6	252	2	D72596	hypothetical prote	506	6	1.6	281	2	G84485	probable Athila re
434	6	1.6	253	2	T46454	hypothetical prote	507	6	1.6	281	2	AC1490	conserved hypotet
435	6	1.6	253	2	H86725	hypothetical prote	508	6	1.6	282	2	H83651	hypothetical prote
436	6	1.6	253	2	T32339	hypothetical prote	509	6	1.6	282	2	C89701	protein F28H6.5 [i
437	6	1.6	254	2	A75173	probable acetylglu	510	6	1.6	283	2	B75263	thiosulfate sulfur
438	6	1.6	254	2	D98560	protein F58A4.1 [i	511	6	1.6	283	2	AE0720	isopentenyl monoph
439	6	1.6	254	2	C55273	hypothetical prote	512	6	1.6	283	2	S27732	conserved hypotet
440	6	1.6	255	2	S39654	probable short-Cha	513	6	1.6	283	2	H71218	probable nicotinat
441	6	1.6	256	2	B69197	conserved hypotet	514	6	1.6	284	2	E72535	probable 4-hydroxy
442	6	1.6	256	2	AH1066	hypothetical prote	515	6	1.6	285	2	S77356	hypothetical prote
443	6	1.6	257	2	A27872	uxu operon transcr	516	6	1.6	285	2	G81442	hypothetical prote
444	6	1.6	257	2	D97093	outer membrane pro	517	6	1.6	285	2	F83259	hypothetical prote
445	6	1.6	257	2	D97093	diguanylate cyclase	518	6	1.6	285	2	S69312	probable membrane
446	6	1.6	258	2	G82122	ParA family protei	519	6	1.6	286	2	AD3263	ribonuclease bn (E
447	6	1.6	258	2	F69455	conserved hypotet	520	6	1.6	287	2	H64588	conserved hypotet
448	6	1.6	258	2	H75349	hypothetical prote	521	6	1.6	287	2	T11959	fatty-acid desatur
449	6	1.6	259	2	AE1102	conserved hypotet	522	6	1.6	287	2	F69413	oxygen-independent
450	6	1.6	259	2	D83557	transcription regu	523	6	1.6	288	2	T35695	probable transcrip
451	6	1.6	260	2	AD2461	hypothetical prote	524	6	1.6	288	2	E86717	hypothetical prote
452	6	1.6	260	2	F97625	hypothetical prote	525	6	1.6	288	2	B40722	homeotic protein 1
453	6	1.6	260	2	B71353	probable D,D-carbo	526	6	1.6	289	1	QQBE4R	EC-RF4 protein - h
454	6	1.6	261	2	S20610	calpastatin - mous	527	6	1.6	289	2	G90314	oxidoreductase [im
455	6	1.6	262	1	E64708	conserved hypotet	528	6	1.6	289	2	G98039	glycerol uptake fa
456	6	1.6	262	2	AH1601	phosphatidate cyti	529	6	1.6	289	2	F95173	glycerol uptake fa
457	6	1.6	262	2	E83463	chemotaxis protein	530	6	1.6	289	2	F71524	hypothetical prote
458	6	1.6	262	2	T46618	probable plasmid p	531	6	1.6	289	2	B83454	cell division prot
459	6	1.6	262	2	A95334	hypothetical prote	532	6	1.6	290	2	B81171	acetyl-CoA carboxy
460	6	1.6	263	2	D83085	conserved hypotet	533	6	1.6	290	2	C81934	probable acetyl-Co
461	6	1.6	263	2	D71342	hypothetical prote	534	6	1.6	291	1	S18718	transcription fact
462	6	1.6	264	2	S24421	dmpH protein - Pse	535	6	1.6	291	2	G69479	methionyl aminopep
463	6	1.6	264	2	F71466	hypothetical prote	536	6	1.6	292	2	G69897	conserved hypotet
464	6	1.6	265	2	H84867	probable endochiti	537	6	1.6	292	2	A70546	probable mena prot
465	6	1.6	265	2	E83599	thiamin biosynthes	538	6	1.6	293	2	AE4110	sugar ABC transpor
466	6	1.6	265	2	A56838	uroporphyrinogen-I	539	6	1.6	293	2	H82184	glycerol-3-phospha
467	6	1.6	265	2	D83761	hypothetical prote	540	6	1.6	293	2	AG3046	transcription regu

541	6	1.6	293	2	E98239	hexA protein (AF05	614	1.6	316	2	S57850	probable NADH2 deh
542	6	1.6	293	2	D84014	hypothetical prote	615	1.6	316	2	KIBSR8	NAM (no apical mer
543	6	1.6	293	2	A12626	transcription regu	616	1.6	317	1	E84636	ribose-phosphate d
544	6	1.6	294	2	B72605	probable high-affi	617	1.6	317	1	S22705	transcription fact
545	6	1.6	294	2	T27417	hypothetical prote	618	1.6	317	2	E82815	ribokinase AF0366
546	6	1.6	294	2	C87449	phenylalanine-4-hy	619	1.6	317	2	S18583	regulatory protein
547	6	1.6	294	2	G71148	probable glycosyl	620	1.6	317	2	AI3617	oxidoreductase (EC
548	6	1.6	295	2	S58285	alpha-soluble NSF	621	1.6	318	1	DNHUN1	NADH2 dehydrogenas
549	6	1.6	295	2	G02238	alpha SNAP - human	622	1.6	318	2	T11833	NADH2 dehydrogenas
550	6	1.6	295	2	S32367	alpha-SNAP protein	623	1.6	318	2	A59153	hypothetical prote
551	6	1.6	295	2	A87415	kinase, GHMP famil	624	1.6	318	2	T02288	hypothetical prote
552	6	1.6	295	2	S61039	hypothetical prote	625	1.6	318	2	T33445	hypothetical prote
553	6	1.6	295	2	A83894	hypothetical prote	626	1.6	318	2	A97676	hypothetical prote
554	6	1.6	295	2	D83734	hypothetical prote	627	1.6	319	2	T35349	hypothetical prote
555	6	1.6	295	2	T40093	hypothetical prote	628	1.6	320	2	T02285	hypothetical prote
556	6	1.6	295	2	H95855	hypothetical prote	629	1.6	320	2	A96570	NAM-like protein,
557	6	1.6	295	2	AB2156	hypothetical prote	630	1.6	321	1	B69687	bo-type ubiquinol
558	6	1.6	296	2	A95962	probable SDR famil	631	1.6	321	2	G95920	probable epimerase
559	6	1.6	296	2	D98345	SN-glycerol-3-phos	632	1.6	322	2	B96014	probable sugar upt
560	6	1.6	296	2	AC2937	hypothetical prote	633	1.6	322	2	T02281	hypothetical prote
561	6	1.6	296	2	C71280	hypothetical prote	634	1.6	322	2	B83579	hypothetical prote
562	6	1.6	296	2	I40328	serum-resistance p	635	1.6	322	2	S28091	hypothetical prote
563	6	1.6	296	2	H90896	hypothetical prote	636	1.6	322	2	T50167	hypothetical prote
564	6	1.6	296	2	S42024	2-haloacid dehalog	637	1.6	322	2	AF2324	bioliverdin reducta
565	6	1.6	296	2	G85720	hypothetical prote	638	1.6	323	2	AD2753	lipoic acid synthet
566	6	1.6	296	2	B64908	ydeH protein - Esc	639	1.6	323	2	B97534	lipoic acid synthet
567	6	1.6	297	2	C83285	probable transcrip	640	1.6	323	2	G83067	hypothetical prote
568	6	1.6	297	2	C83143	hypothetical prote	641	1.6	323	2	D83608	hypothetical prote
569	6	1.6	298	2	D83319	probable transcrip	642	1.6	323	2	H75580	conserved hypothet
570	6	1.6	298	2	T06960	probable membrane	643	1.6	324	2	T35901	quinolate synthet
571	6	1.6	299	2	C90057	hypothetical prote	644	1.6	325	2	T10045	probable arac fami
572	6	1.6	299	2	H97408	probable transcrip	645	1.6	325	2	E70684	hypothetical prote
573	6	1.6	300	2	H84022	arginase rocF limp	646	1.6	325	2	T36562	probable ion-trans
574	6	1.6	300	2	S69052	cytochrome-c oxida	647	1.6	326	2	H82987	magnesium/cohact t
575	6	1.6	300	2	G82975	probable two-compo	648	1.6	326	2	AC2244	hypothetical prote
576	6	1.6	301	2	C35116	hypothetical prote	649	1.6	328	2	AB0021	Laci-family transc
577	6	1.6	301	2	T35163	probable transcrip	650	1.6	328	2	A35257	replication protei
578	6	1.6	302	2	H70523	hypothetical prote	651	1.6	328	2	E85070	hypothetical prote
579	6	1.6	303	2	B43451	Na+/K+-exchangin	652	1.6	328	2	B95861	probable transcrip
580	6	1.6	303	2	A71557	conserved pseudori	653	1.6	328	2	AF2597	hypothetical prote
581	6	1.6	303	2	P69795	conserved hypothet	654	1.6	328	2	H98150	probable transcrip
582	6	1.6	304	1	XMECBD	acetyl-CoA carboxy	655	1.6	329	2	S28442	oligopeptide ABC t
583	6	1.6	304	2	AD0802	acetyl-CoA carboxy	656	1.6	329	2	T36681	exsG protein (AJ22
584	6	1.6	304	2	H91028	acetyl-CoA carboxy	657	1.6	329	2	F98218	probable ATP-bindi
585	6	1.6	304	2	H91028	acetyl-CoA carboxy	658	1.6	329	2	B95900	probable ABC trans
586	6	1.6	305	1	S11663	transcription fact	659	1.6	330	2	H70728	probable atp-bindi
587	6	1.6	305	2	S75743	methionyl aminoep	660	1.6	330	2	F82742	ribosomal large su
588	6	1.6	306	2	C82387	transcription regu	661	1.6	331	2	AE2438	thiamin monophosph
589	6	1.6	306	2	B83723	hypothetical prote	662	1.6	332	2	T32852	hypothetical prote
590	6	1.6	307	2	AD3116	ABC transporter, s	663	1.6	332	2	C75309	delta-aminolevulin
591	6	1.6	307	2	A98171	probable rhizopine	664	1.6	334	2	H95847	probable replicati
592	6	1.6	308	2	S58995	NADH2 dehydrogenas	665	1.6	334	2	H95885	conserved hypothet
593	6	1.6	308	2	B82253	acetyl-CoA carboxy	666	1.6	334	2	AD3089	probable transcrip
594	6	1.6	308	2	AF0997	conserved hypothet	667	1.6	334	2	F98197	hypothetical prote
595	6	1.6	309	2	C72368	hypothetical prote	668	1.6	334	2	T03403	probable serine/th
596	6	1.6	309	2	C96019	probable rhizopine	669	1.6	334	2	T03692	probable serine/th
597	6	1.6	309	2	AC0939	menaquinone biosyn	670	1.6	335	2	AI0295	puative vitamin B1
598	6	1.6	309	2	T46226	hypothetical prote	671	1.6	335	2	A87135	probable membrane
599	6	1.6	309	2	T28708	hypothetical prote	672	1.6	335	2	E12460	hypothetical prote
600	6	1.6	310	2	AH2954	hypothetical prote	673	1.6	335	2	E71215	hypothetical prote
601	6	1.6	311	2	T09656	oryR protein homol	674	1.6	336	2	I39553	glyceraldehyde-3-p
602	6	1.6	311	2	D87164	probable LysR-fami	675	1.6	336	2	S72858	hypothetical prote
603	6	1.6	312	2	AH1456	probable high-affi	676	1.6	336	2	T34783	probable signal pe
604	6	1.6	312	2	E69045	8-oxoguanine DNA g	677	1.6	336	2	G83389	flagellar motor sw
605	6	1.6	313	2	A83951	riboflavin kinase	678	1.6	338	2	G83508	UDP-N-acetylglucos
606	6	1.6	313	2	AB1094	probable high-af	679	1.6	338	2	F84146	hypothetical prote
607	6	1.6	313	2	T48439	probable RNA-bindi	680	1.6	339	2	B72402	hypothetical prote
608	6	1.6	314	2	B70569	conserved hypothet	681	1.6	339	2	T29405	probable transmemb
609	6	1.6	314	2	E87427	probable lppW prot	682	1.6	339	2	T35919	hypothetical prote
610	6	1.6	314	2	D70927	phoE protein U5922	683	1.6	340	2	T47371	hypothetical prote
611	6	1.6	315	2	G97379	hypothetical prote	684	1.6	341	2	F87699	glycosyl transfera
612	6	1.6	315	2	T26422	hypothetical prote	685	1.6	341	2	C72403	hypothetical prote
613	6	1.6	315	2	AD3137	hypothetical prote	686	1.6	341	2		

687	6	1.6	342	2	E64491	N5, N10-methylene	760	6	1.6	360	2	AE1434	mevalonate kinases
688	6	1.6	342	2	S05786	hypothetical prote	761	6	1.6	360	2	I38743	nuclear respirator
689	6	1.6	343	2	A82075	iron(III) dicitrat	762	6	1.6	360	2	C84413	geranylgeranyl hyd
690	6	1.6	343	2	F82755	transcription regu	763	6	1.6	360	2	AB0104	Laci-family regula
691	6	1.6	343	2	T20388	hypothetical prote	764	6	1.6	361	1	S74694	6-phosphofructokin
692	6	1.6	343	2	A98295	ribosomal RNA smal	765	6	1.6	361	2	A75350	phospho-2-dehydro-
693	6	1.6	343	2	T01475	hypothetical prote	766	6	1.6	361	2	D83306	hypothetical prote
694	6	1.6	343	2	C86136	probable enzyme yj	767	6	1.6	361	2	T48538	hypothetical prote
695	6	1.6	343	2	S56595	rRNA (guanine-N2-)	768	6	1.6	361	2	D72721	hypothetical prote
696	6	1.6	343	2	B98267	hypothetical prote	769	6	1.6	361	2	AC1028	probable membrane
697	6	1.6	344	2	T05987	hypothetical prote	770	6	1.6	362	2	D82768	ribonuclease D Xf0
698	6	1.6	344	2	D75311	conserved hypothet	771	6	1.6	362	2	T48564	probable serine ri
699	6	1.6	344	2	E75259	N-acetylmuramoyl-L	772	6	1.6	363	2	S34734	Arp-binding protei
700	6	1.6	344	2	T05730	probable RNA-bind	773	6	1.6	363	2	AB2890	L-lysine 2,3-amino
701	6	1.6	345	1	MMBE17	38.1K membrane pro	774	6	1.6	363	2	G97665	L-lysine 2,3-amino
702	6	1.6	345	2	S22368	NADH2 dehydrogenas	775	6	1.6	363	2	AH2796	hypothetical prote
703	6	1.6	345	2	F70893	probable enoyl-CoA	776	6	1.6	363	2	H97575	probable permease
704	6	1.6	345	2	C55741	thymopoietin gamma	777	6	1.6	363	2	T20608	hypothetical prote
705	6	1.6	345	2	A87338	L-lysine 2,3-amino	778	6	1.6	364	2	H82727	sugar ABC transpor
706	6	1.6	345	2	B83093	probable oxidoredu	779	6	1.6	364	2	F70880	hypothetical prote
707	6	1.6	345	2	S51548	killer toxin K28 -	780	6	1.6	364	2	F84898	hypothetical prote
708	6	1.6	345	2	A70664	hypothetical prote	781	6	1.6	365	2	JC7527	nuclear retroviral
709	6	1.6	346	2	S09539	DNA ligase (ATP) (782	6	1.6	366	2	B87541	sal operon transcr
710	6	1.6	346	2	T35786	transcription regu	783	6	1.6	366	2	D75167	hypothetical prote
711	6	1.6	346	2	S34732	membrane protein -	784	6	1.6	366	2	B82609	hypothetical prote
712	6	1.6	347	2	AB0941	probable ABC trans	785	6	1.6	366	2	E95856	hypothetical sugar
713	6	1.6	347	2	C64105	o-succinylbenzoate	786	6	1.6	366	2	T10352	protein gp41 - Org
714	6	1.6	347	2	C48146	nuclear respirator	787	6	1.6	367	2	T44687	cobalam in biosynth
715	6	1.6	347	2	C40858	GA-binding protei	788	6	1.6	369	2	B43715	protein M homolog
716	6	1.6	347	2	AE2317	hypothetical prote	789	6	1.6	369	2	D81984	riboflavin bifunct
717	6	1.6	347	2	A12310	hypothetical prote	790	6	1.6	369	2	F81178	histone deacetylase
718	6	1.6	348	2	I39490	UDPglucose 4-epime	791	6	1.6	369	2	G75460	hypothetical prote
719	6	1.6	348	2	S23900	nuclear respirator	792	6	1.6	370	2	C70464	Grp-binding protei
720	6	1.6	348	2	I38744	UDPglucose 4-epime	793	6	1.6	370	2	S27344	hupK protein - Rhi
721	6	1.6	349	2	AD0990	probable membrane	794	6	1.6	370	2	T02284	hypothetical prote
722	6	1.6	349	2	F75579	branched-chain ami	795	6	1.6	371	2	T02284	hypothetical prote
723	6	1.6	349	2	S61414	DNA-binding protei	796	6	1.6	372	2	S23326	gene ML2.2 protein
724	6	1.6	349	2	AE3068	two component sens	797	6	1.6	373	2	AC0253	ribonuclease III (
725	6	1.6	350	2	S49551	Enn protein - Stre	798	6	1.6	373	2	T15480	hypothetical prote
726	6	1.6	350	2	D84923	probable exonuclea	799	6	1.6	373	2	F86382	hypothetical prote
727	6	1.6	351	1	S76613	N-acetyl-gamma-glu	800	6	1.6	373	2	C82546	two-component syst
728	6	1.6	351	1	D84430	probable acid phos	801	6	1.6	373	2	A13491	acyltransferase (E
729	6	1.6	351	2	E45229	opsin, blue-sensit	802	6	1.6	374	2	G97692	Grp-binding protei
730	6	1.6	351	2	AE2979	aldo/keto reductas	803	6	1.6	374	2	A83070	conserved hypothet
731	6	1.6	351	2	H98303	hypothetical prote	804	6	1.6	374	2	T34435	hypothetical prote
732	6	1.6	351	2	B97273	uncharacterized pr	805	6	1.6	375	2	G81878	probable lipoprote
733	6	1.6	352	2	T48903	wax synthase [impo	806	6	1.6	376	1	G69336	conserved hypothet
734	6	1.6	353	2	F95403	probable oxidoredu	807	6	1.6	376	2	B84360	citrate synthase (
735	6	1.6	353	2	H83482	hypothetical prote	808	6	1.6	376	2	T07131	probable amino aci
736	6	1.6	353	2	E84393	D-lactate dehydrog	809	6	1.6	376	2	F75503	conserved hypothet
737	6	1.6	354	2	A46393	Grp-binding protei	810	6	1.6	376	2	I39582	nitrite reductase
738	6	1.6	354	2	T38306	guanine nucleotide	811	6	1.6	376	2	AH3209	conserved hypothet
739	6	1.6	354	2	B70663	probable PPE prote	812	6	1.6	377	2	A83275	hypothetical prote
740	6	1.6	354	2	D75460	MoxR-related prote	813	6	1.6	377	2	T45528	Arp2/3 complex cha
741	6	1.6	354	2	E72640	hypothetical prote	814	6	1.6	377	2	T39434	probable arp2-3 co
742	6	1.6	355	2	AD2918	Grp-binding protei	815	6	1.6	378	2	T26684	hypothetical prote
743	6	1.6	355	2	A48358	ORF355 - Bradyrhiz	816	6	1.6	378	2	E75547	iron-sulfur cofact
744	6	1.6	356	2	E71252	probable glycerol-	817	6	1.6	380	2	G97248	uncharacterized co
745	6	1.6	356	2	T03249	glucan endo-1,3-be	818	6	1.6	380	2	C83473	erythronate-4-phos
746	6	1.6	356	2	A13648	flagellar biosynth	819	6	1.6	381	2	G70626	hypothetical prote
747	6	1.6	356	2	D86408	purine permease li	820	6	1.6	382	2	D69304	probable acyl-CoA
748	6	1.6	356	2	G95875	probable spermidin	821	6	1.6	382	2	AG1310	conserved hypothet
749	6	1.6	357	2	S49166	cysteine proteinas	822	6	1.6	382	2	AF1682	conserved hypothet
750	6	1.6	357	2	J02178	hypothetical 39.8K	823	6	1.6	382	2	B40858	GA-binding protei
751	6	1.6	357	2	T26910	hypothetical prote	824	6	1.6	382	2	T04260	hypothetical prote
752	6	1.6	357	2	A83371	Grp-binding protei	825	6	1.6	383	2	A71650	succinyl-diaminopi
753	6	1.6	358	1	A48952	triacylglycerol li	826	6	1.6	383	2	H90482	conserved hypothet
754	6	1.6	358	2	A82041	hypothetical prote	827	6	1.6	385	2	T07130	probable amino aci
755	6	1.6	358	2	H83554	hypothetical prote	828	6	1.6	385	2	E83506	probable MFS trans
756	6	1.6	359	1	LQBFP37	DNA ligase (ATP) (829	6	1.6	385	2	A81526	hypothetical prote
757	6	1.6	359	2	AE1806	mevalonate kinases	830	6	1.6	386	2	A81328	probable periplasm
758	6	1.6	359	2	E83312	hypothetical prote	831	6	1.6	387	2	T09086	sedoheptulose-bisp
759	6	1.6	359	2	S33317	homoserine dehydro	832	6	1.6	387	2	T38876	probable ribosomal

833	6	1.6	387	2	C75312	branched-chain ami	906	6	1.6	408	2	A55533	intracellular coag
834	6	1.6	387	2	AG2900	conserved hypotet	907	6	1.6	409	1	CTBSPI	site-specific DNA-
835	6	1.6	387	2	T17662	hypothetical prote	908	6	1.6	409	2	T40489	hypothetical prote
836	6	1.6	387	2	E97028	probable amidohydr	909	6	1.6	411	2	C57479	amino acid transpo
837	6	1.6	387	2	AB2344	hypothetical prote	910	6	1.6	411	2	A99742	molybdopter in bios
838	6	1.6	388	2	H84079	L-arabinose ABC tr	911	6	1.6	411	2	D85592	molybdopter in bios
839	6	1.6	388	2	T36402	probable monooxyge	912	6	1.6	411	2	A32352	molybdopter in bios
840	6	1.6	389	2	I49263	potential oncogene	913	6	1.6	412	2	C69188	ammonium transport
841	6	1.6	389	2	A53392	Knt10b protein pre	914	6	1.6	412	2	B97077	probable AAA-famil
842	6	1.6	389	2	T22611	hypothetical prote	915	6	1.6	412	2	A83604	poly A polymerase
843	6	1.6	390	2	T38370	hypothetical prote	916	6	1.6	413	2	G87299	molybdopter in bios
844	6	1.6	390	2	H70904	probable lprK prot	917	6	1.6	413	2	AB0603	hypothetical prote
845	6	1.6	390	2	A83384	N-acetylmuramoyl-L	918	6	1.6	414	2	C75461	F9H16.7 protein -
846	6	1.6	390	2	H87606	conserved hypotet	919	6	1.6	414	2	C86342	transcription fact
847	6	1.6	390	2	AD3213	oxidoeductase Atu	920	6	1.6	414	2	A53950	hypothetical prote
848	6	1.6	393	2	T21335	hypothetical prote	921	6	1.6	416	1	ITSH	hypothetical prote
849	6	1.6	393	2	G83155	probable MFS trans	922	6	1.6	416	2	D21097	alpha-1-antitrypsi
850	6	1.6	393	2	AG0184	probable multidrug	923	6	1.6	416	2	D84638	probable sarcosine
851	6	1.6	394	2	E83213	probable acyl-CoA	924	6	1.6	416	2	T23383	hypothetical prote
852	6	1.6	394	2	P90725	membrane spanning	925	6	1.6	416	2	E95915	probable enzyme, s
853	6	1.6	394	2	D88021	protein W10D9.3 li	926	6	1.6	417	2	S51564	hypothetical prote
854	6	1.6	394	2	G85576	membrane spanning	927	6	1.6	418	2	B87536	membrane protein,
855	6	1.6	395	2	I38741	nuclear respirator	928	6	1.6	418	2	H83126	probable secretin
856	6	1.6	395	2	A98329	hypothetical prote	929	6	1.6	418	2	G82608	conserved hypotet
857	6	1.6	395	2	AD2954	NAD binding oxidor	930	6	1.6	418	2	B83683	hypothetical prote
858	6	1.6	396	1	A40365	siderophore biosyn	931	6	1.6	418	2	T35586	hypothetical prote
859	6	1.6	396	2	B87651	phosphoglycerate k	932	6	1.6	419	2	AH3166	hypothetical prote
860	6	1.6	396	2	B57479	amino acid transpo	933	6	1.6	420	2	F70842	hypothetical prote
861	6	1.6	396	2	AH3375	serine-type D-Ala-	934	6	1.6	420	2	T36072	hypothetical prote
862	6	1.6	397	2	H84097	histidyl-tRNA synt	935	6	1.6	421	2	C83147	hypothetical prote
863	6	1.6	397	2	A96681	hypothetical prote	936	6	1.6	421	2	A83039	gamma-glutamyl pho
864	6	1.6	397	2	G84247	atrazine chlorohyd	937	6	1.6	421	2	JVU057	conserved hypotet
865	6	1.6	397	2	S09813	hypothetical prote	938	6	1.6	422	1	KXHUZ	tolA protein - Bsc
866	6	1.6	397	2	T23026	hypothetical prote	939	6	1.6	422	2	A36403	plasma protein Z p
867	6	1.6	397	2	T23642	hypothetical prote	940	6	1.6	423	2	AG1973	ferrochelatase (EC
868	6	1.6	398	2	H72257	hypothetical prote	941	6	1.6	423	2	AB1034	hypothetical prote
869	6	1.6	398	2	H81141	hypothetical prote	942	6	1.6	424	2	AC0182	UV protection prot
870	6	1.6	398	2	S74347	hypothetical prote	943	6	1.6	424	2	D97833	molybdopter in bios
871	6	1.6	399	1	A55578	cytochrome P450 -	944	6	1.6	425	2	S04848	hypothetical prote
872	6	1.6	399	2	A75269	acetyl-CoA acetyl	945	6	1.6	426	2	C99831	transcription init
873	6	1.6	399	2	A47755	pectic enzyme secr	946	6	1.6	426	2	T31490	conserved hypotet
874	6	1.6	400	2	JC2473	doc2 protein - hum	947	6	1.6	427	2	A13490	membrane-bound lyl
875	6	1.6	401	2	T19771	hypothetical prote	948	6	1.6	428	2	T39847	dihydroorotase (EC
876	6	1.6	401	2	AB0864	probable aminotran	949	6	1.6	428	2	B96781	hypothetical prote
877	6	1.6	401	2	F91087	hypothetical prote	950	6	1.6	428	2	GBHUA	unknown protein f9
878	6	1.6	401	2	H85932	hypothetical prote	951	6	1.6	429	2	F87417	serine hydroxymeth
879	6	1.6	401	2	F65063	Cysteine sulfinate	952	6	1.6	429	2	S49595	probable serine pr
880	6	1.6	401	2	B82951	probable MFS trans	953	6	1.6	429	2	AE0406	arsenical pump mem
881	6	1.6	402	2	T09062	probable advanced	954	6	1.6	429	2	F84015	maltose/maltodextr
882	6	1.6	403	2	AI1371	multi-drug resista	955	6	1.6	429	2	D69635	H+/Na+-glutamate s
883	6	1.6	403	2	AG1741	multi-drug resista	956	6	1.6	429	2	A97241	permease (imported
884	6	1.6	403	2	AI0699	probable pathogeni	957	6	1.6	429	2	F86240	hypothetical prote
885	6	1.6	403	2	C90045	hypothetical prote	958	6	1.6	430	2	AH0394	probable amino aci
886	6	1.6	404	2	C46665	aspartate kinase (959	6	1.6	430	2	E82583	threonine synthase
887	6	1.6	404	2	D69455	pantothenate metab	960	6	1.6	430	2	T36892	NADH2 dehydrogenas
888	6	1.6	404	2	F81724	conserved hypotet	961	6	1.6	431	2	B98162	hypothetical prote
889	6	1.6	404	2	AF0034	probable integral	962	6	1.6	431	2	D87608	serum and glucocor
890	6	1.6	405	1	F69611	cytochrome P450 cy	963	6	1.6	431	2	A48094	hypothetical prote
891	6	1.6	405	2	D81918	sodium-translocati	964	6	1.6	432	2	T34154	hypothetical prote
892	6	1.6	405	2	G81184	Na(+)-translocati	965	6	1.6	432	2	T35263	probable carboxype
893	6	1.6	405	2	A57479	amino acid transpo	966	6	1.6	432	2	D86937	probable membrane
894	6	1.6	405	2	S38348	5-carboxymethyl-2-	967	6	1.6	432	2	G69977	two-component sens
895	6	1.6	405	2	T42992	cyclin D - Caenorh	968	6	1.6	432	2	G64662	hypothetical prote
896	6	1.6	405	2	T26678	hypothetical prote	969	6	1.6	433	2	E71853	hypothetical prote
897	6	1.6	405	2	F64076	tyrosine-specific	970	6	1.6	433	2	F87256	cytochrome P450 fa
898	6	1.6	406	2	H70364	iron-sulfur cofact	971	6	1.6	434	2	T35055	probable transport
899	6	1.6	406	2	A83104	probable hydrolase	972	6	1.6	436	2	AI1015	probable exported
900	6	1.6	406	2	H70670	hypothetical prote	973	6	1.6	436	2	S56054	CUS1 protein - yea
901	6	1.6	407	2	A69188	ammonium transport	974	6	1.6	436	2	H47070	probable O-antigen
902	6	1.6	407	2	E69409	conserved hypotet	975	6	1.6	437	2	H87294	probable domain
903	6	1.6	407	2	C82327	MSHA biogenesis pr	976	6	1.6	437	2	AD2469	two-component hybr
904	6	1.6	407	2	D95882	probable efflux pr	977	6	1.6	437	2		
905	6	1.6	408	2	G87646	molybdopter in bios	978	6	1.6	437	2		

979 6 1.6 438 2 A55070 DNA primase (EC 2.
 980 6 1.6 439 2 C6392 hypothetical prote
 981 6 1.6 440 2 T47906 FUSCA PROTEIN FUS6
 982 6 1.6 440 2 G83195 probable amino aci
 983 6 1.6 440 2 AD2628 ABC transporter, m
 984 6 1.6 440 2 C97410 hypothetical prote
 985 6 1.6 440 2 S71795 transcription fact
 986 6 1.6 441 2 S60247 platelet-activatin
 987 6 1.6 441 2 F86595 CT700 hypothetical
 988 6 1.6 441 2 G72029 conserved hypothet
 989 6 1.6 443 1 S29334 transcription fact
 990 6 1.6 444 2 C83336 probable cytochrom
 991 6 1.6 444 2 T20374 hypothetical prote
 992 6 1.6 444 2 AH0346 putative HlyD fami
 993 6 1.6 445 1 A49447 transcription fact
 994 6 1.6 445 1 S31224 transcription fact
 995 6 1.6 446 2 F70302 transporter (pho87
 996 6 1.6 446 2 G70774 probable atpH prot
 997 6 1.6 448 2 A69959 glycine dehydrogen
 998 6 1.6 450 2 A38171 L-lysine 6-transam
 999 6 1.6 450 2 B70506 hypothetical prote
 1000 6 1.6 452 2 D83609 probable glutamine

ALIGNMENTS

RESULT 1
 H33627
 hypothetical protein PA0144 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: H83627
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83627
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-208 <STO>
 A:Cross-references: UNIPROT:Q916Y8; GB:AE004452; GB:AE004091; NID:G9945968; PIDN:AAG0353
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0144
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC191.05c

Query Match 2.1%; Score 8; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 TFLRLAAL 203
 |||||
 Db 12 TFLRLAAL 19

RESULT 2
 H69995
 hypothetical protein ytlr - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: H69995
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galle
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelld

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69995
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-309 <KUN>
 A:Cross-references: UNIPROT:O34799; GB:Z99119; GB:AL009126; NID:G2635411; PIDN:CAB14972.1
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ytlr

Query Match 2.1%; Score 8; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 MHEVVGSL 91
 |||||
 Db 73 MHEVVGSL 80

RESULT 3
 A33616
 heterogeneous ribonuclear particle protein L - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
 C:Accession: A33616
 R:Pinol-Roma, S.; Swanson, M.S.; Gall, J.G.; Dreyfuss, G.
 J. Cell Biol. 109, 2575-2587, 1989
 A:Title: A novel heterogeneous nuclear RNP protein with a unique distribution on nascent
 A:Reference number: A33616; MUID:90078296; PMID:2687284
 A:Accession: A33616
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-558 <PIN>
 A:Cross-references: UNIPROT:PI4866; GB:X16135; NID:G32355; PIDN:CAA34261.1; PID:G32356
 C:Superfamily: Caenorhabditis elegans hypothetical protein C44B7.2

Query Match 2.1%; Score 8; DB 2; Length 558;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 221 KTPASPVV 228
 |||||
 Db 66 KTPASPVV 73

RESULT 4
 T34180
 hypothetical protein C49H3.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34180
 R:Wu, X.
 submitted to the EMBL Data Library, December 1995
 A:Description: The sequence of C. elegans cosmid C49H3.
 A:Reference number: Z21485

A:Accession: T34180
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-812 <WUX>
 A:Cross-references: EMBL:U42436; PIDN:AAA83485.1; CESP:C49H3.5
 C:Genetics:
 A:Gene: CESP:C49H3.5
 A:Introns: 12/3; 35/3; 67/3; 174/3; 208/3; 266/2; 288/1; 310/3; 539/2; 633/3

Query Match 2.1%; Score 8; DB 2; Length 812;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ABAEISFT 50
|||||
DB 217 ABAEISFT 224

RESULT 5

B34106
protein kinase (EC 2.7.1.37), cGMP-dependent 2, type 1 [similarity] - fruit fly (Drosophila)
N:Contains: protein kinase, cGMP-dependent 2, type 3; protein kinase, cGMP-dependent 2,
C:Species: Drosophila melanogaster
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: B34106; E34106; F34106
R:Kaiderson, D.; Rubin, G.M.
J. Biol. Chem. 264, 10738-10748, 1989
A:Title: cGMP-dependent protein kinase genes in Drosophila.
A:Reference number: A34106; MUID:89278147; PMID:2732245
A:Accession: B34106
A:Molecule type: DNA; mRNA
A:Residues: 1-1088 <KAL>
A:Cross-references: UNIPROT:Q03043; GB:M27117; GB:M27118; GB:M27119; GB:M27120; NID:gl57
A:Note: the authors translated the codon AGG for residue 692 as Thr
A:Accession: E34106
A:Status: not compared with conceptual translation
A:Molecule type: DNA; mRNA
A:Residues: 347-507, 'S', 508-691, 'T', 693-1088 <KA2>
A:Accession: F34106
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA; mRNA
A:Residues: 521-691, 'T', 693-1088 <KA3>
C:Genetics:
A:Gene: FlyBase:for
A:Cross-references: FlyBase:FBgn0000721
C:Keywords: alternative splicing; ATP; cGMP binding; phosphotransferase; serine/threonine
F:347-1088/Product: protein kinase, cGMP-dependent 2, type 3 #status predicted <TV3>
F:520-637/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP1>
F:521-1088/Product: protein kinase, cGMP-dependent 2, type cD4 #status predicted <CD4>
F:638-762/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP2>
F:775-1036/Domain: protein kinase homology <KIN>
F:783-791/Region: protein kinase ATP-binding motif

Query Match 2.1%; Score 8; DB 2; Length 1088;

Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 HTASGLRL 163

DB 235 HTASGLRL 242
|||||

RESULT 6

C64331
ribosomal protein S27 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64331
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64331
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <BUL>
A:Cross-references: UNIPROT:P54028; GB:U67480; GB:L77117; NID:g2826265; PIDN:AA898237.1;
C:Genetics:
A:Map position: FOR235984-236172
C:Superfamily: rat ribosomal protein S27

Query Match 1.8%; Score 7; DB 2; Length 62;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 PRGGK GK 29

DB 46 PRGGK GK 52
|||||

RESULT 7

AF3030
hypothetical protein Atu3850 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF3030
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF3030
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <KUR>
A:Cross-references: UNIPROT:Q8U978; GB:AE008689; PIDN:AAL44660.1; PID:g17742285; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3850
A:Map position: linear chromosome

Query Match 1.8%; Score 7; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GRLAYLP 214

DB 19 GRLAYLP 25
|||||

RESULT 8

T27015
hypothetical protein Y48E1B.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27015
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20299
A:Accession: T27015
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-89 <WIL>
A:Cross-references: UNIPROT:O18200; EMBL:Z933393; PIDN:CAB07692.1; GSPDB:GN00020; CESP:Y48
A:Experimental source: clone Y48E1B
C:Genetics:
A:Gene: CESP:Y48E1B.6
A:Map position: 2
A:Introns: 10/1; 44/3

Query Match 1.8%; Score 7; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VVMSGDG 82

DB 35 VVMSGDG 41
|||||

RESULT 9

H98254
hypothetical protein AGR_L_1980 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H98254
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <KUR>
A;Cross-references: UNIPROT:Q8U978; GB:AE007870; PIDN:AAK89562.1; PID:gl5159447; GSPDB:C
C;Genetics:
A;Gene: AGR_L1980
A;Map position: linear chromosome

Query Match 1.8%; Score 7; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 GRLAYLP 214
Db 29 GRLAYLP 35
|||||

RESULT 10
I68726
Ige chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K. Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid sequences of the C region and the C domain
A;Reference number: I54443; MUID:88152907; PMID:3346043
A;Accession: I68726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:M22930; NID:gl94455; PIDN:AAA37911.1; PID:gl94460
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>

Query Match 1.8%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 VDLESEK 183
Db 32 VDLESEK 38
|||||

RESULT 11
I68730
Ige chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K. Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid sequences of the C region and the C domain
A;Reference number: I54443; MUID:88152907; PMID:3346043
A;Accession: I68730
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:M22933; NID:gl94464; PIDN:AAA37915.1; PID:gl94469
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>

Query Match 1.8%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 VDLESEK 183
Db 32 VDLESEK 38
|||||

RESULT 12
S50770
hypothetical protein YJL215c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRE119; hypothetical protein J0231
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S50770; S57005; S45158
R;Vandenbol, M.; Durand, P.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F. Yeast 10, 1657-1662, 1994
A;Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of yeast chromosome V
A;Reference number: S50701; MUID:95242842; PMID:7725802
A;Accession: S50770
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-119 <VAN>
A;Cross-references: UNIPROT:P40895; EMBL:Z34098; NID:9496934; PIDN:CAA83996.1; PID:949694
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995
A;Reference number: S56835
A;Accession: S57005
A;Molecule type: DNA
A;Residues: 1-119 <VAN>
A;Cross-references: EMBL:Z49490; NID:gl015601; PIDN:CAA89512.1; PID:gl015602; MIPS:YJL215
C;Genetics:
A;Cross-references: SGD:S0003751
A;Map position: 10L
C;Superfamily: Saccharomyces hypothetical protein YJL215c

Query Match 1.8%; Score 7; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LLNPRGG 26
Db 102 LLNPRGG 108
|||||

RESULT 13
G75308
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75308
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <WHI>
A;Cross-references: UNIPROT:Q9RSG8; GB:AE002049; GB:AE000513; NID:g6459945; PIDN:AAF11710
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2156
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR2156

Query Match 1.8%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 ADVDES 181

Fri Jun 17 16:34:19 2005

Db 27 ADVLES 33
|||||

RESULT 14

S25119
histone H2A - Trypanosoma cruzi
C:Species: Trypanosoma cruzi
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25119; S33211
R:Lopez, M.C.
submitted to the EMBL Data Library, July 1992
A:Reference number: S25119
A:Accession: S25119
A:Molecule type: DNA
A:Residues: 1-135 <LOP>
A:Cross-references: EMBL:X67287; NID:g10617; PIDN:CAA47703.1; PID:g10618
C:Superfamily: histone H2A
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 1.8%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 PVGRVGS 220

Db 28 PVGRVGS 34
|||||

RESULT 15

C45051
lamprin 2 precursor, long splice form - sea lamprey
N:Alternate names: lamprin L-0.9-12
N:Contains: lamprin 2 precursor, short splice form (lamprin L-0.9-10)
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 09-Jul-2004
C:Accession: C45051; A45051
R:Robson, P.; Wright, G.M.; Sitarz, E.; Maiti, A.; Rawat, M.; Youson, J.H.; Keeley, F.W.
J. Biol. Chem. 268, 1440-1447, 1993
A:Title: Characterization of lamprin, an unusual matrix protein from lamprey cartilage.
A:Reference number: A45051; MUID:93123269; PMID:7678258
A:Accession: C45051
A:Molecule type: mRNA
A:Residues: 1-139 <ROB>
A:Cross-references: UNIPROT:P33575; GB:L05925; NID:g213209; PIDN:AAA49269.1; PID:g213210
A:Note: sequence extracted from NCBI backbone (NCBIP:122170)
A:Accession: A45051
A:Molecule type: mRNA
A:Residues: 1-85,105-139 <RO2>
A:Cross-references: GB:L05924; NID:g213207; PIDN:AAA49268.1; PID:g213208
A:Note: sequence extracted from NCBI backbone (NCBIP:122166)
C:Comment: These forms are encoded by a different gene than B45051; we have arbitrarily
C:Superfamily: lamprin
C:Keywords: alternative splicing; cartilage; extracellular matrix
P:1-19/Domain: signal sequence #status predicted <SIG>
F:1-19/Product: lamprin 2, long splice form #status predicted <MAT1>
F:20-85,105-139/Product: lamprin 2, short splice form #status predicted <MAT2>

Query Match 1.8%; Score 7; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 LVLALLH 265

Db 9 LVLALLH 15
|||||

Search completed: June 15, 2005, 12:22:56
Job time : 67 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 12:03:24 ; Search time 163 Seconds
(without alignments)
911.141 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 384
Sequence: 1 MDPAGGPGVLPKPCVRLVL.....CVERPPSNKQMPPEPL 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	384	4	AAB48007 Human sph
2	384	100.0	384	7	ADF28783 Human sph
3	336	87.5	384	3	AAB18659 A human r
4	336	87.5	384	4	AAB94589 Human pro
5	336	87.5	384	4	AAB93955 Human pro
6	336	87.5	384	4	AAB00924 Human sph
7	336	87.5	384	5	ABG31586 Human sph
8	336	87.5	384	7	ADP38365 Human pro
9	333	86.7	398	8	ADJ75441 Marker ge
10	333	86.7	398	8	ADJ75387 Marker ge
11	333	86.7	398	8	ADO22417 Human sph
12	320	83.3	368	6	ABR82391 Human sph
13	287	74.7	384	6	ABP71054 Human sph
14	285	74.2	333	5	ABP90209 Human pol
15	257	66.9	305	4	AAM41966 Human pol
16	250	65.1	384	5	ABB08089 Human sph
17	250	65.1	384	8	ADQ17905 Human sof
18	235	61.2	384	3	AAY96057 Human sph
19	235	61.2	384	4	AM40180 Human pol
20	209	54.4	293	2	AAW88613 Secreted
21	209	54.4	293	4	ABB50380 Human sec
22	209	54.4	293	6	ABO44637 Novel hum
23	209	54.4	293	7	ABO26117 Human pro
24	144	37.5	384	4	AAE07882 Human sph
25	138	35.9	138	5	AAU75327 Human sph

127	33.1	138	5	AAU75344	Human sph
127	33.1	138	5	AAU75338	Human sph
126	32.8	138	5	AAU75345	Human sph
124	22.3	138	5	AAU75346	Human sph
107	27.9	204	5	ABB08095	Human sph
31	25.3	138	5	AAU75343	Human sph
32	24.7	138	5	AAU75350	Human sph
32	24.7	138	5	AAU75342	Human sph
34	22.7	138	5	AAU75341	Human sph
35	22.7	138	5	AAU75349	Human sph
36	20.8	80	4	AAE00925	Conserved
37	19.3	138	5	AAU75339	Human sph
38	19.3	138	5	AAU75347	Human sph
39	19.0	138	5	AAU75340	Human sph
40	19.0	138	5	AAU75348	Human sph
41	18.5	138	5	AAU75337	Human sph
42	18.5	138	5	AAU75336	Human sph
43	14.3	119	4	ABB50835	Human sec
44	14.3	119	6	ABO45092	Novel hum
45	14.3	119	7	ABO26572	Protein a
46	8.6	138	5	AAU75328	Mouse sph
47	8.6	260	4	ABU52807	Human sig
48	8.6	373	5	ABB08091	Murine sp
49	8.6	381	3	AAV56053	Mouse sph
50	8.6	381	5	ABB08087	Murine sp
51	8.6	382	5	ABB08090	Murine sp
52	8.6	382	4	AAE07883	Mouse con
53	8.6	382	5	ABG31588	Mouse sph
54	8.6	388	3	AAV56054	Mouse sph
55	8.6	388	5	ABB08088	Murine sp
56	8.6	388	8	ADJ76219	Marker ge
57	5.2	20	4	AAE00928	Peptide 2
58	5.2	20	4	AAE00927	Peptide 1
59	5.2	20	4	AAE00929	Peptide 3
60	4.9	80	4	AAE00933	Conserved
61	4.4	160	4	ABU52808	Human sig
62	4.2	16	4	AAE00926	Signature
63	3.4	14	7	ADF28773	Human sph
64	3.4	80	4	AAE00992	Consensus
65	3.1	21	4	AAE00930	Peptide 4
66	2.9	11	7	ADF28774	Human sph
67	2.6	10	7	ADF28772	Human sph
68	2.3	114	4	AAE04370	Human kin
69	2.3	232	5	ABP41247	Human ova
70	2.3	244	4	AAV93260	Human pol
71	2.3	244	8	ADL30678	Human pro
72	2.3	456	4	ABG21143	Novel hum
73	2.3	618	4	AAU09074	Human sph
74	2.3	618	4	AAU09075	Human sph
75	2.3	618	5	ABG31587	Human sph
76	2.3	618	5	ABB07855	Protein s
77	2.3	618	7	ADP38417	Human pro
78	2.3	618	8	ADQ15182	Human can
79	2.3	654	4	ABU52806	Human sig
80	2.3	654	8	ADJ66569	Sphingos
81	2.3	806	4	ABG21144	Novel hum
82	2.1	140	6	ABU05297	Human dia
83	2.1	150	2	AAV60549	Human nor
84	2.1	208	8	ADL14814	Pseudomon
85	2.1	225	7	ABO79900	Pseudomon
86	2.1	288	4	AAE05758	Mycobacte
87	2.1	292	3	ABU23014	Protein e
88	2.1	301	6	ABR82390	D. melano
89	2.1	524	6	ABR82390	D. melano
90	2.1	558	6	ABO52974	Novel hum
91	2.1	567	4	ABG15420	Novel hum
92	2.1	589	4	AAU27959	Human con
93	2.1	589	4	AAU27787	Human ful
94	2.1	589	5	ABR97144	Human tum
95	2.1	624	4	AAU33004	Novel hum
96	2.1	757	7	ABO83795	Pseudomon
97	2.1	907	4	ABB57980	Drosophil
98	2.1	907	6	ABR82393	D. melano

99	8	2.1	1088	4	ABE67108	Abb567108 Drosophil	172	7	1.8	343	5	AAU80295	Aau80295 Murine Ig
100	8	2.1	1088	8	ADQ89698	Adq89698 Antagonis	173	7	1.8	353	5	AAE22659	Aae22659 Hamster a
101	8	2.1	1178	6	ABM70281	Abm70281 Photorhab	174	7	1.8	354	5	ABG60939	Abg60939 Novel flo
102	101	7	23	8	ADK01659	Adk01659 Hepatitis	175	7	1.8	364	8	ADN21160	Adn21160 Bacterial
103	7	1.8	24	4	ABE50836	Abb50836 Human sec	176	7	1.8	369	7	ADM05113	Adm05113 Human pro
104	7	1.8	24	6	ABO45093	Abb45093 Human sec	177	7	1.8	375	4	AAU52280	Aau52280 Propionib
105	7	1.8	24	7	ABO26573	Abb26573 Protein a	178	7	1.8	375	6	ABM48799	Abm48799 Propionib
106	7	1.8	25	2	AAW00041	Aaw00041 Tibial gr	179	7	1.8	376	7	ABO68516	Abb68516 Pseudomon
107	7	1.8	28	4	AAO08226	Aao08226 Human pol	180	7	1.8	377	7	ABO74962	Abb74962 Pseudomon
108	7	1.8	56	5	ABG77125	Abg77125 Prostate	181	7	1.8	388	6	AAE35111	Aae35111 Mouse imm
109	7	1.8	58	4	AAU41853	Aau41853 Propionib	182	7	1.8	388	6	AAE35111	Aae35111 Mouse imm
110	7	1.8	58	6	ABM38372	Abm38372 Propionib	183	7	1.8	393	4	AAU27871	Aau27871 Fruit fly
111	7	1.8	62	7	ADC89332	Adc89332 Ribosomal	184	7	1.8	399	6	ABU38825	Abu38825 Protein e
112	7	1.8	66	4	AAU65010	Aau65010 Propionib	185	7	1.8	401	6	ADA35675	Ada35675 Acinetoba
113	7	1.8	66	6	ABM61529	Abm61529 Propionib	186	7	1.8	410	6	ABU25823	Abu25823 Protein e
114	7	1.8	71	2	AAW38743	Aaw38743 S. pneumo	187	7	1.8	410	7	ABO73826	Abb73826 Pseudomon
115	7	1.8	71	4	AAO05659	Aao05659 Human pol	188	7	1.8	410	7	ABO83970	Abb83970 Pseudomon
116	7	1.8	71	6	ABP75758	Abp75758 Human sec	189	7	1.8	421	5	AAU80300	Aau80300 Mouse Ige
117	7	1.8	87	8	ADR96324	Adr96324 Novel S.	190	7	1.8	421	6	ABP96586	Abp96586 Mouse Ige
118	7	1.8	106	4	AAU44856	Aau44856 Propionib	191	7	1.8	421	6	AAE35016	Aae35016 Mouse imm
119	7	1.8	106	6	ABM411375	Abm411375 Propionib	192	7	1.8	422	2	AAE51269	Aae51269 Human NRS
120	7	1.8	117	7	ADM41873	Adm41873 Human ant	193	7	1.8	422	2	AAE43651	Aae43651 Rat NRSF.
121	7	1.8	119	7	ADM41875	Adm41875 Human ant	194	7	1.8	422	2	AAE68568	Aae68568 Rat NDF.
122	7	1.8	135	7	ABO78399	Abb78399 Pseudomon	195	7	1.8	422	2	AAE68569	Aae68569 Rat NDF e
123	7	1.8	138	5	AAU75329	Aau75329 Human sph	196	7	1.8	423	6	AAE35112	Aae35112 Mouse imm
124	7	1.8	138	5	AAU75330	Aau75330 Mouse sph	197	7	1.8	426	6	ABU26229	Abu26229 Aspergill
125	7	1.8	161	4	AAU57160	Aau57160 Propionib	198	7	1.8	427	4	ABB65442	Abb65442 Drosophil
126	7	1.8	161	6	ABM53679	Abm53679 Propionib	199	7	1.8	432	5	AAU80294	Aau80294 Murine Ig
127	7	1.8	167	2	AAE14362	Aae14362 E.histoly	200	7	1.8	440	3	ABU49487	Abu49487 Protein e
128	7	1.8	181	6	ABE56752	Abb56752 Human sec	201	7	1.8	442	3	AAE53178	Aae53178 Macaca mu
129	7	1.8	185	6	ABU01128	Abu01128 S. pneumo	202	7	1.8	452	6	ABU31727	Abu31727 Protein e
130	7	1.8	185	8	ABU46286	Abu46286 Streptoco	203	7	1.8	457	6	ABR44268	Abu44268 Novel hum
131	7	1.8	200	7	ABO74601	Abb74601 Pseudomon	204	7	1.8	457	8	ADN23655	Adn23655 Bacterial
132	7	1.8	210	4	ABE58746	Abb58746 Drosophil	205	7	1.8	459	6	ABM72925	Abm72925 Staphyloc
133	7	1.8	211	7	ABO76763	Abb76763 Pseudomon	206	7	1.8	461	2	AAE68572	Aae68572 Rat NDF e
134	7	1.8	217	5	AAE16241	Aae16241 Tomato in	207	7	1.8	461	2	AAE68571	Aae68571 Rat NDF e
135	7	1.8	221	6	ABU49978	Abu49978 Protein e	208	7	1.8	461	2	AAE66718	Aae66718 Human acy
136	7	1.8	221	8	AGC32240	Adg32240 Mutant B_	209	7	1.8	463	7	ABO66317	Abb66317 Klebsiell
137	7	1.8	236	7	ABO73552	Abb73552 Pseudomon	210	7	1.8	470	5	ABP30175	Abp30175 Streptoco
138	7	1.8	242	8	ADS22876	Ads22876 Bacterial	211	7	1.8	476	5	ABP26844	Abp26844 Streptoco
139	7	1.8	251	4	AAE25293	Aam25293 Human pro	212	7	1.8	496	5	ABB57052	Abb57052 Mouse isc
140	7	1.8	254	7	ADM26770	Adm26770 Hyperther	213	7	1.8	497	8	ADJ78520	Adj78520 Human gly
141	7	1.8	255	3	AGC04469	Aeg04469 Arabidops	214	7	1.8	508	8	ADS44935	Ads44935 Bacterial
142	7	1.8	256	7	ABO81287	Abb81287 Pseudomon	215	7	1.8	518	4	ABE59352	Abb59352 Drosophil
143	7	1.8	257	6	ABU38869	Abu38869 Protein e	216	7	1.8	519	5	ABP26845	Abp26845 Streptoco
144	7	1.8	259	5	AAE16232	Aae16232 Tomato in	217	7	1.8	536	4	ABE71168	Abb71168 Drosophil
145	7	1.8	261	7	ABO74740	Abb74740 Pseudomon	218	7	1.8	561	2	AAE17415	Aae17415 Mouse imm
146	7	1.8	262	3	AGC39893	Aeg39893 Arabidops	219	7	1.8	562	4	AAE40687	Aae40687 Human pol
147	7	1.8	272	3	AAE40468	Aeg40468 Arabidops	220	7	1.8	571	5	ABE48363	Abb48363 Listeria
148	7	1.8	277	6	ABU12106	Abu12106 Human pro	221	7	1.8	574	8	ADN19927	Adn19927 Bacterial
149	7	1.8	281	8	ADK72308	Adk72308 Human Apo	222	7	1.8	581	7	ADJ21588	Adj21588 Novel hum
150	7	1.8	282	4	ABG10942	Abg10942 Novel hum	223	7	1.8	586	6	ABU16803	Abu16803 Protein e
151	7	1.8	285	6	ABR53300	Abf53300 Protein s	224	7	1.8	586	7	ADC00965	Adc00965 Enterohae
152	7	1.8	285	7	ADK63546	Adk63546 Disease t	225	7	1.8	586	8	ADR86289	Adr86289 Aspergill
153	7	1.8	288	6	ABO00541	Abb00541 Novel hum	226	7	1.8	592	2	AAW38337	Aaw38337 Bovine br
154	7	1.8	298	4	ABE67747	Abb67747 Amino aci	227	7	1.8	602	8	ADN21189	Adn21189 Bacterial
155	7	1.8	299	4	ABG00168	Abg00168 Novel hum	228	7	1.8	604	6	ADA33180	Ada33180 Acinetoba
156	7	1.8	299	6	ABG71247	Abg71247 Human cra	229	7	1.8	605	7	ADC86971	Adc86971 Human GPC
157	7	1.8	306	5	ABE49527	Abb49527 Listeria	230	7	1.8	616	6	ABE68566	Abm68566 Photorhab
158	7	1.8	306	7	ABO62228	Abb62228 Klebsiell	231	7	1.8	617	4	AAU09073	Aau09073 Mouse sph
159	7	1.8	313	3	ABY79997	Abf79997 Mouse imm	232	7	1.8	618	7	ADD14179	Add14179 Human src
160	7	1.8	315	6	ABJ25629	Abj25629 Aspergill	233	7	1.8	636	2	AAE68576	Aae68576 Rat NDF e
161	7	1.8	316	4	AAU56112	Aam56112 Propionib	234	7	1.8	636	2	AAE68573	Aae68573 Rat NDF e
162	7	1.8	316	6	ABM52631	Abm52631 Propionib	235	7	1.8	639	2	AAE68574	Aae68574 Rat NDF e
163	7	1.8	320	7	ABG75191	Abg75191 M licheni	236	7	1.8	639	2	AAE68578	Aae68578 Rat NDF e
164	7	1.8	328	2	AAW05504	Aaw05504 HCMV Tole	237	7	1.8	646	4	ABE67103	Abb67103 Drosophil
165	7	1.8	330	6	AAU20156	Aau20156 Protein e	238	7	1.8	662	2	AAE68577	Aae68577 Rat NDF e
166	7	1.8	332	5	AAU80298	Aau80298 Murine Ig	239	7	1.8	662	7	ADE62015	Ade62015 Rat Prote
167	7	1.8	332	5	AAU80299	Aau80299 Murine Ig	240	7	1.8	662	7	ADE62019	Ade62019 Rat Prote
168	7	1.8	332	5	AAU80297	Aau80297 Mouse Ige	241	7	1.8	662	7	ADE62003	Ade62003 Rat Prote
169	7	1.8	338	8	ADR08817	Adr08817 Human pro	242	7	1.8	662	7	ADE62007	Ade62007 Rat Prote
170	7	1.8	342	7	ABO61894	Abb61894 Klebsiell	243	7	1.8	662	7	ADD48428	Add48428 Rat Prote
171	7	1.8	343	5	AAU80296	Aau80296 Murine Ig	244	7	1.8	662	7	ADE62011	Ade62011 Rat Prote

245	7	1.8	666	7	ADH88274	Adh88274 Enterococ	318	6	1.6	9	8	ADK84387	Adk84387 Human 191
246	7	1.8	683	8	ADO77831	Ado77831 Rat synap	319	6	1.6	9	8	ADK87019	Adk87019 Human 191
247	7	1.8	683	8	ADP44592	Adp44592 Norway ra	320	6	1.6	9	8	ADK87274	Adk87274 Human 191
248	7	1.8	684	8	ADP44592	Adp44592 Norway ra	321	6	1.6	9	8	ADK88373	Adk88373 Human 191
249	7	1.8	684	8	ADP44592	Adp44592 Norway ra	322	6	1.6	9	8	ADK88508	Adk88508 Human 191
250	7	1.8	694	8	ADH89399	Adh89399 AXMI-007	323	6	1.6	9	8	ADK88031	Adk88031 Human 191
251	7	1.8	695	4	ADP67746	Adp67746 Amino aci	324	6	1.6	9	8	ADK87979	Adk87979 Human 191
252	7	1.8	700	4	ADP67745	Adp67745 Amino aci	325	6	1.6	9	8	ADK87248	Adk87248 Human 191
253	7	1.8	715	3	ADP51002	Adp51002 C. vicina	326	6	1.6	9	8	ADK88400	Adk88400 Human 191
254	7	1.8	717	5	ADP27165	Adp27165 Streptoco	327	6	1.6	9	8	ADK84418	Adk84418 Human 191
255	7	1.8	719	6	ADU22328	Adu22328 Protein e	328	6	1.6	9	8	ADK87453	Adk87453 Human 191
256	7	1.8	733	6	ADU46769	Adu46769 Protein e	329	6	1.6	9	8	ADK83338	Adk83338 Human 191
257	7	1.8	744	8	ADH89397	Adh89397 AXMI-007	330	6	1.6	9	8	ADK84902	Adk84902 Human 191
258	7	1.8	804	7	ADP72930	Adp72930 Pseudomon	331	6	1.6	9	8	ADK83331	Adk83331 Human 191
259	7	1.8	829	7	ADP75272	Adp75272 Pseudomon	332	6	1.6	9	8	ADK87024	Adk87024 Human 191
260	7	1.8	855	4	ADP67757	Adp67757 Amino aci	333	6	1.6	9	8	ADK88542	Adk88542 Human 191
261	7	1.8	874	5	ADP46769	Adp46769 Synchocy	334	6	1.6	9	8	ADK8436	Adk8436 Cat aller
262	7	1.8	896	5	ADP808760	Adp808760 Synchoco	335	6	1.6	9	8	ADK8763	Adk8763 Cat aller
263	7	1.8	903	5	ADP46793	Adp46793 Synchoco	336	6	1.6	9	8	ADK88542	Adk88542 Human 191
264	7	1.8	921	7	ADP46793	Adp46793 Synchoco	337	6	1.6	9	8	ADK88542	Adk88542 Human 191
265	7	1.8	955	6	ADP81200	Adp81200 Arabidops	338	6	1.6	9	8	ADK88542	Adk88542 Human 191
266	7	1.8	1001	4	ADP81200	Adp81200 Arabidops	339	6	1.6	9	8	ADK88542	Adk88542 Human 191
267	7	1.8	1035	5	ADP81200	Adp81200 Arabidops	340	6	1.6	9	8	ADK88542	Adk88542 Human 191
268	7	1.8	1069	3	ADP81200	Adp81200 Arabidops	341	6	1.6	9	8	ADK88542	Adk88542 Human 191
269	7	1.8	1080	7	ADP81200	Adp81200 Arabidops	342	6	1.6	9	8	ADK88542	Adk88542 Human 191
270	7	1.8	1116	4	ADP81200	Adp81200 Arabidops	343	6	1.6	9	8	ADK88542	Adk88542 Human 191
271	7	1.8	1116	8	ADP81200	Adp81200 Arabidops	344	6	1.6	9	8	ADK88542	Adk88542 Human 191
272	7	1.8	1183	6	ADP81200	Adp81200 Arabidops	345	6	1.6	9	8	ADK88542	Adk88542 Human 191
273	7	1.8	1207	6	ADP81200	Adp81200 Arabidops	346	6	1.6	9	8	ADK88542	Adk88542 Human 191
274	7	1.8	1212	6	ADP81200	Adp81200 Arabidops	347	6	1.6	9	8	ADK88542	Adk88542 Human 191
275	7	1.8	1212	5	ADP81200	Adp81200 Arabidops	348	6	1.6	9	8	ADK88542	Adk88542 Human 191
276	7	1.8	1213	5	ADP81200	Adp81200 Arabidops	349	6	1.6	9	8	ADK88542	Adk88542 Human 191
277	7	1.8	1224	5	ADP81200	Adp81200 Arabidops	350	6	1.6	9	8	ADK88542	Adk88542 Human 191
278	7	1.8	1225	5	ADP81200	Adp81200 Arabidops	351	6	1.6	9	8	ADK88542	Adk88542 Human 191
279	7	1.8	1253	3	ADP81200	Adp81200 Arabidops	352	6	1.6	9	8	ADK88542	Adk88542 Human 191
280	7	1.8	1253	6	ADP81200	Adp81200 Arabidops	353	6	1.6	9	8	ADK88542	Adk88542 Human 191
281	7	1.8	1260	7	ADP81200	Adp81200 Arabidops	354	6	1.6	9	8	ADK88542	Adk88542 Human 191
282	7	1.8	1266	7	ADP81200	Adp81200 Arabidops	355	6	1.6	9	8	ADK88542	Adk88542 Human 191
283	7	1.8	1266	8	ADP81200	Adp81200 Arabidops	356	6	1.6	9	8	ADK88542	Adk88542 Human 191
284	7	1.8	1268	3	ADP81200	Adp81200 Arabidops	357	6	1.6	9	8	ADK88542	Adk88542 Human 191
285	7	1.8	1268	4	ADP81200	Adp81200 Arabidops	358	6	1.6	9	8	ADK88542	Adk88542 Human 191
286	7	1.8	1268	7	ADP81200	Adp81200 Arabidops	359	6	1.6	9	8	ADK88542	Adk88542 Human 191
287	7	1.8	1282	5	ADP81200	Adp81200 Arabidops	360	6	1.6	9	8	ADK88542	Adk88542 Human 191
288	7	1.8	1297	3	ADP81200	Adp81200 Arabidops	361	6	1.6	9	8	ADK88542	Adk88542 Human 191
289	7	1.8	1300	3	ADP81200	Adp81200 Arabidops	362	6	1.6	9	8	ADK88542	Adk88542 Human 191
290	7	1.8	1310	6	ADP81200	Adp81200 Arabidops	363	6	1.6	9	8	ADK88542	Adk88542 Human 191
291	7	1.8	1319	2	ADP81200	Adp81200 Arabidops	364	6	1.6	9	8	ADK88542	Adk88542 Human 191
292	7	1.8	1333	3	ADP81200	Adp81200 Arabidops	365	6	1.6	9	8	ADK88542	Adk88542 Human 191
293	7	1.8	1333	3	ADP81200	Adp81200 Arabidops	366	6	1.6	9	8	ADK88542	Adk88542 Human 191
294	7	1.8	1333	7	ADP81200	Adp81200 Arabidops	367	6	1.6	9	8	ADK88542	Adk88542 Human 191
295	7	1.8	1333	7	ADP81200	Adp81200 Arabidops	368	6	1.6	9	8	ADK88542	Adk88542 Human 191
296	7	1.8	1333	7	ADP81200	Adp81200 Arabidops	369	6	1.6	9	8	ADK88542	Adk88542 Human 191
297	7	1.8	1333	7	ADP81200	Adp81200 Arabidops	370	6	1.6	9	8	ADK88542	Adk88542 Human 191
298	7	1.8	1333	7	ADP81200	Adp81200 Arabidops	371	6	1.6	9	8	ADK88542	Adk88542 Human 191
299	7	1.8	1336	2	ADP81200	Adp81200 Arabidops	372	6	1.6	9	8	ADK88542	Adk88542 Human 191
300	7	1.8	1357	6	ADP81200	Adp81200 Arabidops	373	6	1.6	9	8	ADK88542	Adk88542 Human 191
301	7	1.8	1357	6	ADP81200	Adp81200 Arabidops	374	6	1.6	9	8	ADK88542	Adk88542 Human 191
302	7	1.8	1368	5	ADP81200	Adp81200 Arabidops	375	6	1.6	9	8	ADK88542	Adk88542 Human 191
303	7	1.8	1440	7	ADP81200	Adp81200 Arabidops	376	6	1.6	9	8	ADK88542	Adk88542 Human 191
304	7	1.8	1549	4	ADP81200	Adp81200 Arabidops	377	6	1.6	9	8	ADK88542	Adk88542 Human 191
305	7	1.8	1549	4	ADP81200	Adp81200 Arabidops	378	6	1.6	9	8	ADK88542	Adk88542 Human 191
306	7	1.8	1571	8	ADP81200	Adp81200 Arabidops	379	6	1.6	9	8	ADK88542	Adk88542 Human 191
307	7	1.8	1742	8	ADP81200	Adp81200 Arabidops	380	6	1.6	9	8	ADK88542	Adk88542 Human 191
308	7	1.8	1892	5	ADP81200	Adp81200 Arabidops	381	6	1.6	9	8	ADK88542	Adk88542 Human 191
309	7	1.8	2045	4	ADP81200	Adp81200 Arabidops	382	6	1.6	9	8	ADK88542	Adk88542 Human 191
310	7	1.8	3745	6	ADP81200	Adp81200 Arabidops	383	6	1.6	9	8	ADK88542	Adk88542 Human 191
311	7	1.8	9234	7	ADP81200	Adp81200 Arabidops	384	6	1.6	9	8	ADK88542	Adk88542 Human 191
312	6	1.6	9	2	ADP81200	Adp81200 Arabidops	385	6	1.6	9	8	ADK88542	Adk88542 Human 191
313	6	1.6	9	2	ADP81200	Adp81200 Arabidops	386	6	1.6	9	8	ADK88542	Adk88542 Human 191
314	6	1.6	9	8	ADP81200	Adp81200 Arabidops	387	6	1.6	9	8	ADK88542	Adk88542 Human 191
315	6	1.6	9	8	ADP81200	Adp81200 Arabidops	388	6	1.6	9	8	ADK88542	Adk88542 Human 191
316	6	1.6	9	8	ADP81200	Adp81200 Arabidops	389	6	1.6	9	8	ADK88542	Adk88542 Human 191
317	6	1.6	9	8	ADP81200	Adp81200 Arabidops	390	6	1.6	9	8	ADK88542	Adk88542 Human 191

391	6	1.6	19	4	ABG53582	Human liv	464	6	1.6	45	4	AAM96506	Human rep
392	6	1.6	19	5	ABG411713	Human pep	465	6	1.6	47	4	ABG26791	Novel hum
393	6	1.6	20	4	ABU52809	Human sig	466	6	1.6	48	3	AAB63150	Human imm
394	6	1.6	21	3	AY922778	O. aureus	467	6	1.6	48	4	AAM88280	Human sec
395	6	1.6	21	6	ABU54855	Human CA1	468	6	1.6	48	4	AAM94841	Human rep
396	6	1.6	22	2	AAW72378	L0L2 zinc	469	6	1.6	50	7	ADE09292	Novel pro
397	6	1.6	22	7	ADD25751	Binding d	470	6	1.6	51	3	AY92783	Vtgs8-bet
398	6	1.6	25	2	ABR14208	Signal pe	471	6	1.6	51	3	AY92779	Vtgs8-CrF
399	6	1.6	25	6	ABP72517	Oncostati	472	6	1.6	51	4	AAM23533	Human EST
400	6	1.6	26	4	ABB38637	Peptide #	473	6	1.6	51	4	AAU14936	Novel bon
401	6	1.6	26	4	AAM32096	Peptide #	474	6	1.6	51	4	AAU47827	Propionib
402	6	1.6	26	4	AAW71811	Human bon	475	6	1.6	51	4	AAU39620	Propionib
403	6	1.6	26	4	AAM59268	Human bra	476	6	1.6	51	6	ABM44346	Propionib
404	6	1.6	26	4	ABG53495	Human liv	477	6	1.6	51	6	ABM36139	Propionib
405	6	1.6	26	5	ABG41624	Human pep	478	6	1.6	53	4	AAM88359	Human imm
406	6	1.6	28	4	ABG28687	Peptide #	479	6	1.6	53	4	AAM94442	Human rep
407	6	1.6	28	4	AAM67042	Human bon	480	6	1.6	53	4	ABB10779	Human ova
408	6	1.6	28	4	AAM54636	Human bra	481	6	1.6	53	4	AAU65342	Propionib
409	6	1.6	28	4	ABG48707	Human liv	482	6	1.6	53	4	AAM65342	Human ova
410	6	1.6	28	4	AAM02627	Peptide #	483	6	1.6	53	5	ABP02637	Human foe
411	6	1.6	29	2	AAW10846	MAB anti-	484	6	1.6	53	5	ABP04271	Human ORF
412	6	1.6	31	6	ABJ18847	Human Bcl	485	6	1.6	53	6	ABM61861	Propionib
413	6	1.6	31	8	ABO57930	Human gen	486	6	1.6	54	4	AAM72506	Human bon
414	6	1.6	33	2	AAW10861	MAB anti-	487	6	1.6	54	4	AAM59912	Human bra
415	6	1.6	33	3	ABB34492	Human sec	488	6	1.6	54	4	ABG54197	Human liv
416	6	1.6	34	3	AY922780	Vtgs8-CAT	489	6	1.6	54	4	ABG08249	Novel hum
417	6	1.6	35	4	AAW17644	Peptide #	490	6	1.6	54	4	AAU31806	Novel hum
418	6	1.6	35	4	ABB36664	Peptide #	491	6	1.6	54	5	ABG42326	Human pep
419	6	1.6	35	4	AAM30162	Peptide #	492	6	1.6	54	6	ADA95347	Protein d
420	6	1.6	35	4	ABB31451	Peptide #	493	6	1.6	55	4	AAO09035	Human pol
421	6	1.6	35	4	ABB22000	Protein #	494	6	1.6	55	4	AAU59749	Propionib
422	6	1.6	35	4	AAM69823	Human bon	495	6	1.6	55	6	ABM56268	Propionib
423	6	1.6	35	4	AAM57427	Human bra	496	6	1.6	56	4	ABB37443	Peptide #
424	6	1.6	35	4	ABG51514	Human liv	497	6	1.6	56	4	ABB32192	Peptide #
425	6	1.6	35	4	AAO55302	Peptide #	498	6	1.6	56	4	AAM70564	Human bon
426	6	1.6	35	5	ABG39450	Human pep	499	6	1.6	56	4	AAM58121	Human bra
427	6	1.6	36	4	AAU01651	Human sec	500	6	1.6	56	4	ABG52245	Human liv
428	6	1.6	36	5	ABG77131	Prostate	501	6	1.6	56	5	AAE20276	Human lun
429	6	1.6	36	5	AAO18839	K28 kille	502	6	1.6	57	2	AY12337	Human 5'
430	6	1.6	36	6	ADA04638	IGF-1R b1	503	6	1.6	57	4	AAB80373	Secreted
431	6	1.6	36	7	ADH95851	Insulin g	504	6	1.6	57	4	AAU80400	Secreted
432	6	1.6	36	8	ADL68542	IGF-1R/IR	505	6	1.6	57	4	AAU45019	Propionib
433	6	1.6	36	8	ADM38387	Insulin a	506	6	1.6	57	5	ABP09755	Human ORF
434	6	1.6	38	3	AY92782	Vtgs8-EGF	507	6	1.6	57	5	ABG5265	Human alb
435	6	1.6	38	4	AAW18773	Peptide #	508	6	1.6	57	5	ABG5264	Human alb
436	6	1.6	38	4	ABB37874	Peptide #	509	6	1.6	57	6	ABM41538	Propionib
437	6	1.6	38	4	AAM31281	Peptide #	510	6	1.6	57	8	ADL78532	Albumin f
438	6	1.6	38	4	ABB23132	Protein #	511	6	1.6	57	8	ADL78531	Albumin f
439	6	1.6	38	4	AAW71003	Human bon	512	6	1.6	57	8	ABO60603	Human gen
440	6	1.6	38	4	AAM58505	Human bra	513	6	1.6	58	4	AAW13728	Peptide #
441	6	1.6	38	4	ABG52720	Human liv	514	6	1.6	58	4	ABB32663	Peptide #
442	6	1.6	38	5	ABG40793	Human pep	515	6	1.6	58	4	AAM26132	Peptide #
443	6	1.6	39	3	AY44777	N-termina	516	6	1.6	58	4	AAM84884	Human imm
444	6	1.6	39	4	AAM21562	Peptide #	517	6	1.6	58	4	ABB27510	Human pep
445	6	1.6	39	4	ABB43914	Peptide #	518	6	1.6	58	4	ABB18160	Protein #
446	6	1.6	39	4	AAM37836	Peptide #	519	6	1.6	58	4	AAU42606	Propionib
447	6	1.6	39	4	ABE26832	Protein #	520	6	1.6	58	4	AAU42606	Propionib
448	6	1.6	39	4	AAM77640	Human bon	521	6	1.6	58	4	AAM53489	Human bra
449	6	1.6	39	4	AAM64904	Human bra	522	6	1.6	58	4	ABG47516	Human liv
450	6	1.6	39	4	ABG59289	Human liv	523	6	1.6	58	4	AAW01481	Peptide #
451	6	1.6	39	5	ABG46672	Human pep	524	6	1.6	58	5	ABG35504	Human pep
452	6	1.6	39	8	ABO54337	Human gen	525	6	1.6	58	5	ABP35315	Human ORF
453	6	1.6	40	5	ABP30840	Streptoco	526	6	1.6	58	6	ABM39125	Propionib
454	6	1.6	40	5	ABP30843	Streptoco	527	6	1.6	59	3	AAG28165	Arabidops
455	6	1.6	40	5	ABP30842	Streptoco	528	6	1.6	59	4	AAM80699	Human hae
456	6	1.6	40	5	ABP30845	Streptoco	529	6	1.6	59	4	AAW81275	Human hae
457	6	1.6	40	5	ABP30844	Streptoco	530	6	1.6	59	4	AAW80710	Human hae
458	6	1.6	40	5	ABP30841	Streptoco	531	6	1.6	59	4	AAW81370	Human hae
459	6	1.6	40	5	ABP30839	Streptoco	532	6	1.6	59	4	AAW80461	Human hae
460	6	1.6	41	3	AAW25745	Human sec	533	6	1.6	59	4	AAW80705	Human hae
461	6	1.6	44	7	ADF60339	Human con	534	6	1.6	59	4	AAW81101	Human hae
462	6	1.6	45	3	ABG08842	Arabidops	535	6	1.6	60	6	ADA33355	Acinetoba
463	6	1.6	45	4	ABW12194	Human PRO	536	6	1.6	61	8	ABO54568	Human gen

537	6	1.6	62	2	AAV59916	AAV59916 Human nor	610	6	1.6	74	5	ABG76944	Abg76944 Human pro
538	6	1.6	62	3	ABB62913	Aab62913 Human ebg	611	6	1.6	74	6	ABR47612	AbR47612 Breast ca
539	6	1.6	62	4	AAU66614	Aau66614 Propionib	612	6	1.6	74	7	ADB75583	ADB75583 Prostate
540	6	1.6	62	5	ABP06544	Abp06544 Human ORF	613	6	1.6	74	7	ADN39995	Adn39995 Cancer/an
541	6	1.6	62	6	ABM64852	Abm64852 Propionib	614	6	1.6	74	7	ADN39144	Adn39144 Cancer/an
542	6	1.6	62	6	ABM63133	Abm63133 Propionib	615	6	1.6	74	7	ADN95458	Adn95458 Human BEC
543	6	1.6	64	3	AGG00477	Aag00477 Human sec	616	6	1.6	74	8	ADL56806	Adl56806 Human SEC
544	6	1.6	64	3	AGG28497	Aag28497 Zee mays	617	6	1.6	74	8	ADO39190	Ado39190 Human nov
545	6	1.6	64	4	AAO13904	Aao13904 Human pol	618	6	1.6	75	3	AAG33735	Aag33735 Arabidops
546	6	1.6	64	8	ABO57973	Abos7973 Human gen	619	6	1.6	75	4	AA856067	Aab56067 Skin cell
547	6	1.6	65	3	AA856204	Aab56204 Human sec	620	6	1.6	75	4	AA856042	Aam93042 Human dig
548	6	1.6	65	4	AAW21190	Aam21190 Peptide #	621	6	1.6	75	5	AB872267	Abu72267 Murine pr
549	6	1.6	65	4	AB843511	Abb43511 Peptide #	622	6	1.6	76	4	AAU54468	Aau54468 Propionib
550	6	1.6	65	4	AAW37405	Aam37405 Peptide #	623	6	1.6	76	4	ABG20486	Abg20486 Novel hum
551	6	1.6	65	4	AB826671	Abm26671 Protein #	624	6	1.6	76	5	ABP34802	Abp34802 Human ATP
552	6	1.6	65	4	AAW77254	Aam77254 Human bon	625	6	1.6	76	6	ABM50987	Abm50987 Propionib
553	6	1.6	65	4	AAU44249	Aau44249 Propionib	626	6	1.6	76	6	ABU35356	Abu35356 Proteoin e
554	6	1.6	65	4	AAU54559	Aau54559 Propionib	627	6	1.6	77	4	AAU52195	Aau52195 Propionib
555	6	1.6	65	4	AAW64448	Aam64448 Human bra	628	6	1.6	77	4	ABG20862	Abg20862 Novel hum
556	6	1.6	65	4	ABG58890	Abg58890 Human liv	629	6	1.6	77	6	ABM48714	Abm48714 Propionib
557	6	1.6	65	5	ABG46270	Abg46270 Human pep	630	6	1.6	78	3	AAV76030	Aay76030 Murine ek
558	6	1.6	65	6	ABP77092	Abp77092 N. gonorr	631	6	1.6	78	3	AAV75980	Aay75980 Murine ek
559	6	1.6	65	6	ABM40768	Abm40768 Propionib	632	6	1.6	78	3	AA856348	Aab56348 Human sec
560	6	1.6	65	6	ABM51078	Abm51078 Propionib	633	6	1.6	78	4	AA855969	Aab55969 Skin cell
561	6	1.6	65	8	ADP29285	Adp29285 Human sec	634	6	1.6	78	4	AA855919	Aab55919 Skin cell
562	6	1.6	65	8	ADP29286	Adp29286 Human sec	635	6	1.6	78	4	AAU50098	Aau50098 Propionib
563	6	1.6	66	5	ABP05666	Abp05666 Human ORF	636	6	1.6	78	4	ABG11290	Abg11290 Novel hum
564	6	1.6	67	3	AA828164	Aag28164 Arabidops	637	6	1.6	78	4	AAU32442	Aau32442 Novel hum
565	6	1.6	67	5	AB881416	Abb81416 Human pro	638	6	1.6	78	4	AAU33135	Aau33135 Novel hum
566	6	1.6	67	8	ADG74892	Adg74892 Plant dev	639	6	1.6	78	5	ABB72119	Abb72119 Murine pr
567	6	1.6	68	3	AB858757	Aab58757 Breast an	640	6	1.6	78	5	ABB72169	Abb72169 Murine pr
568	6	1.6	68	4	AAU39406	Aau39406 Propionib	641	6	1.6	78	6	ADA20815	Ada20815 Wheat ada
569	6	1.6	68	5	ABP34301	Abp34301 Human ORF	642	6	1.6	78	6	ADA20815	Ada20815 Wheat ada
570	6	1.6	68	6	ABM35925	Abm35925 Propionib	643	6	1.6	78	6	ABO62418	Abo62418 Klebsiell
571	6	1.6	68	7	ADF04600	Adf04600 Bacterial	644	6	1.6	78	7	ABO62418	Abo62418 Klebsiell
572	6	1.6	68	7	ABO62654	Abo62654 Klebsiell	645	6	1.6	79	2	AAW06936	Aaw06936 Cagi locu
573	6	1.6	69	4	AAO01923	Aao01923 Human pol	646	6	1.6	79	2	AAW06936	Aaw06936 Cagi locu
574	6	1.6	70	3	AG333091	Aag33091 Zee mays	647	6	1.6	79	5	ABP06766	Abp06766 Human ORF
575	6	1.6	70	4	AAW21289	Aam21289 Peptide #	648	6	1.6	79	5	ABP42284	Abp42284 Human ova
576	6	1.6	70	4	AB868981	Abb68981 Drosophil	649	6	1.6	80	2	AAV48258	Aay48258 Human pro
577	6	1.6	70	4	AB843622	Abb43622 Peptide #	650	6	1.6	80	2	AAV48258	Aay48258 Human pro
578	6	1.6	70	4	AAW37516	Aam37516 Peptide #	651	6	1.6	80	2	AAV48551	Aay48551 Human bre
579	6	1.6	70	4	AAW77366	Aam77366 Human bon	652	6	1.6	80	3	AA87886	Aam87886 Human imm
580	6	1.6	70	4	AAW44563	Aam44563 Human bra	653	6	1.6	80	4	AAW87062	Aam87062 Human imm
581	6	1.6	70	4	ABG58999	Abg58999 Human liv	654	6	1.6	80	4	AAW24511	Aam24511 C886P pre
582	6	1.6	70	5	ABG46380	Abg46380 Human pep	655	6	1.6	80	4	ABM16321	Abm16321 Human ner
583	6	1.6	70	7	ABO66027	Abo66027 Klebsiell	656	6	1.6	80	4	ABG21055	Abg21055 Novel hum
584	6	1.6	72	4	AAO06452	Aao06452 Human pol	657	6	1.6	80	6	ABP55360	Abp55360 Human col
585	6	1.6	72	5	AB853109	Abb53109 Human ORF	658	6	1.6	80	6	ABP55360	Abp55360 Human col
586	6	1.6	72	7	ADI60245	Adi60245 Secreted	659	6	1.6	81	2	AAW06550	Aaw06550 Human col
587	6	1.6	73	4	AAU14798	Aau14798 Novel bon	660	6	1.6	81	2	AAW46882	Aaw46882 Protein s
588	6	1.6	73	4	AAU62673	Aau62673 Propionib	661	6	1.6	81	5	ABP11152	Abp11152 Human ORF
589	6	1.6	73	5	AAE16434	Aae16434 Human int	662	6	1.6	81	5	AAU76210	Aau76210 Human col
590	6	1.6	73	5	ABP32358	Abp32358 Human ORF	663	6	1.6	81	5	ABG32039	Abg32039 Human col
591	6	1.6	73	6	ABR39513	AbR39513 Human int	664	6	1.6	81	6	ABU02888	Abu02888 S. pneumo
592	6	1.6	73	6	ABM59192	Abm59192 Propionib	665	6	1.6	81	8	ADU58732	Adu58732 Human col
593	6	1.6	73	6	ABR57362	AbR57362 Human int	666	6	1.6	82	2	AA827371	Aar27371 TRFP Chai
594	6	1.6	73	6	ABP58028	Abp58028 Human int	667	6	1.6	82	4	AAU39226	Aau39226 Propionib
595	6	1.6	73	6	ABP97946	Abp97946 Amino aci	668	6	1.6	82	6	ABM35745	Abm35745 Propionib
596	6	1.6	73	6	ABR58060	AbR58060 Human int	669	6	1.6	82	6	ABO44366	AbO44366 Corn 3-be
597	6	1.6	73	6	ABU62033	Abu62033 Human int	670	6	1.6	82	7	ADF60545	Adf60545 Human con
598	6	1.6	73	7	ADD84722	Add84722 Human int	671	6	1.6	83	2	AA883119	Aar883119 Human cis
599	6	1.6	73	7	ADM17261	Adm17261 Human int	672	6	1.6	83	4	AAU27714	Aau27714 Human ful
600	6	1.6	73	7	ADM29238	Adm29238 Human int	673	6	1.6	83	4	AAW23636	Aam23636 Human EST
601	6	1.6	73	8	ADH41331	Adh41331 Human int	674	6	1.6	84	4	ABB17576	Abb17576 Human ner
602	6	1.6	73	8	ADG48094	Adg48094 Human int	675	6	1.6	84	6	ABO00644	AbO00644 Novel hum
603	6	1.6	73	8	ADI53000	Adi53000 Human int	676	6	1.6	84	7	ABO70294	Abo70294 Pseudomon
604	6	1.6	73	8	ADK01648	Adk01648 Hepatitis	677	6	1.6	85	4	AAO05191	Aao05191 Human pol
605	6	1.6	73	8	ADR46719	Adr46719 Human Irf	678	6	1.6	85	7	ADM26741	Adm26741 Hyperther
606	6	1.6	74	2	AA826876	Aar26876 Human int	679	6	1.6	85	8	ABO57692	AbO57692 Human gen
607	6	1.6	74	2	AAW27631	Aaw27631 Human int	680	6	1.6	86	3	AA858961	Aab58961 Breast an
608	6	1.6	74	3	AAV99888	Aay99888 Human int	681	6	1.6	86	4	AAO08397	Aao08397 Human pol
609	6	1.6	74	5	ABP07318	Abp07318 Human ORF	682	6	1.6	86	4	AAU56654	Aau56654 Propionib

683	6	1.6	86	6	ABM53173	Abm53173 Propionib	756	6	1.6	97	6	ABO00929	Abo00929 Polypepti
684	6	1.6	86	6	ABO00884	Abo00884 Polypepti	757	6	1.6	97	6	ABU70489	Abu70489 Human adi
685	6	1.6	86	8	ADR28032	ADR28032 Murine IG	758	6	1.6	97	6	ABU70553	Abu70553 Human adi
686	6	1.6	87	4	AAm18705	AAm18705 Peptide #	759	6	1.6	97	7	ABO76762	AbO76762 Pseudomon
687	6	1.6	87	4	AAm23666	AAm23666 Human EST	760	6	1.6	97	8	ADK02046	Adk02046 Hepatitis
688	6	1.6	87	4	AAO06891	AAO06891 Human pol	761	6	1.6	97	8	ADO21109	Ado21109 Human car
689	6	1.6	87	4	AAO01133	AAO01133 Human pol	762	6	1.6	98	3	ABG62911	Abg62911 Human sbg
690	6	1.6	87	4	ABG16805	ABG16805 Novel hum	763	6	1.6	98	3	ABB71225	Abb71225 Drosophil
691	6	1.6	88	3	AAg08720	AAg08720 Arabidops	764	6	1.6	98	4	AAg71708	Ag71708 Human olf
692	6	1.6	88	3	AAg43353	AAg43353 Arabidops	765	6	1.6	98	4	ABG09326	Abg09326 Novel hum
693	6	1.6	88	3	AAO08666	AAO08666 Human pol	766	6	1.6	99	8	ADP29919	Adp29919 Human sec
694	6	1.6	88	4	AAU45366	AAU45366 Propionib	767	6	1.6	100	3	AAg33711	Aag33711 Arabidops
695	6	1.6	88	5	ABP33519	ABP33519 Human ORF	768	6	1.6	100	3	AAg04492	Aag04492 Arabidops
696	6	1.6	88	6	ABM41885	ABM41885 Propionib	769	6	1.6	100	4	AAm01316	Aam01316 P100C pa
697	6	1.6	89	4	ABG26799	ABG26799 Novel hum	770	6	1.6	100	4	AAU69961	Aau69961 Human pro
698	6	1.6	90	2	AAy49886	AAy49886 Arabidops	771	6	1.6	100	4	ABU71852	Abu71852 Prostate
699	6	1.6	90	3	AAg09289	AAg09289 Arabidops	772	6	1.6	100	5	ABB90160	Abb90160 Human pol
700	6	1.6	90	3	AAg08663	AAg08663 Arabidops	773	6	1.6	100	5	ABB95421	Abb95421 Human P10
701	6	1.6	90	4	AAU07708	AAU07708 Rat Kv2.1	774	6	1.6	100	5	ABU05758	Abu05758 M. tuberc
702	6	1.6	90	4	AAU07537	AAU07537 Rat Kv2.1	775	6	1.6	100	5	ABR54533	Abr54533 Prostate
703	6	1.6	90	4	AAU030492	AAU030492 Novel hum	776	6	1.6	100	7	ADB14383	AdB14383 Human pro
704	6	1.6	90	5	ABP39698	ABP39698 Staphyloc	777	6	1.6	100	7	ADG26799	Adg26799 Human pro
705	6	1.6	90	6	ADA12044	ADA12044 Human nov	778	6	1.6	100	8	ADR28031	Adr28031 Murine NC
706	6	1.6	90	7	ADL33307	ADL33307 Human tra	779	6	1.6	101	2	AAr27372	Aar27372 TRFP Chai
707	6	1.6	90	8	ADK01921	ADK01921 Hepatitis	780	6	1.6	101	4	ABG10366	Abg10366 Novel hum
708	6	1.6	90	8	ADS07465	ADS07465 Staphyloc	781	6	1.6	101	4	ABG10366	Abg10366 Novel hum
709	6	1.6	91	4	AAg73730	AAg73730 Human col	782	6	1.6	101	5	ABP05739	Abp05739 Human ORF
710	6	1.6	91	4	AAm94107	AAm94107 Human rep	783	6	1.6	101	5	ABP42039	Abp42039 Human ova
711	6	1.6	91	4	AAU30427	AAU30427 Novel hum	784	6	1.6	101	7	ADC87846	Adc87846 Ribosomal
712	6	1.6	92	2	AAr411983	AAr411983 Human T c	785	6	1.6	102	3	ABG62909	Abg62909 Human sbg
713	6	1.6	92	2	AAr36539	AAr36539 TRFP chai	786	6	1.6	102	4	ABB71608	Abb71608 Drosophil
714	6	1.6	92	2	AAy25595	AAy25595 Cat aller	787	6	1.6	102	4	ABG67894	Abg67894 Human cyt
715	6	1.6	92	5	ABP10357	ABP10357 Human ORF	788	6	1.6	102	4	ABG50507	Abg50507 Human pro
716	6	1.6	92	5	ABP04312	ABP04312 Human ORF	789	6	1.6	102	4	ABG26896	Abg26896 Novel hum
717	6	1.6	92	5	ABP98885	ABP98885 Reverse t	790	6	1.6	102	5	ABU05676	Abu05676 M. tuberc
718	6	1.6	92	7	ADC34845	ADC34845 Cat aller	791	6	1.6	102	7	ADL12447	Adl12447 PDZ ligand
719	6	1.6	92	8	ADP29289	ADP29289 Human sec	792	6	1.6	102	8	ADL04969	Adl04969 M. catarr
720	6	1.6	92	8	ADP29287	ADP29287 Human sec	793	6	1.6	103	4	ABG16106	Abg16106 Novel hum
721	6	1.6	93	4	AAO10271	AAO10271 Human pol	794	6	1.6	103	5	ABP43539	Abp43539 Human sec
722	6	1.6	93	5	ABB79263	ABB79263 Human pro	795	6	1.6	104	5	ABP32685	Abp32685 Human ORF
723	6	1.6	93	6	ABP54176	ABP54176 Human lun	796	6	1.6	104	8	ADU08646	Adu08646 Human pro
724	6	1.6	94	2	AAr12119	AAr12119 TRFP chai	797	6	1.6	105	4	AAU86559	Aau86559 Novel hum
725	6	1.6	94	2	AAr27367	AAr27367 TRFP Chai	798	6	1.6	105	4	AAg75553	Aag75553 Human col
726	6	1.6	94	3	AAy51468	AAy51468 Human TRF	799	6	1.6	105	4	AAm90625	Aam90625 Human imm
727	6	1.6	94	3	AAy51473	AAy51473 Human TRF	800	6	1.6	105	7	ADBS9893	AdB59893 Connectiv
728	6	1.6	94	3	AAb28931	AAb28931 T cell re	801	6	1.6	105	7	ADB65134	AdB65134 Human pro
729	6	1.6	94	3	AAb28980	AAb28980 T cell re	802	6	1.6	105	8	ADL53469	AdL53469 Human PDZ
730	6	1.6	94	3	AAy90101	AAy90101 Cat TRFP	803	6	1.6	105	8	ADM33560	Adm33560 Human PDZ
731	6	1.6	94	3	AAy87671	AAy87671 Feline hu	804	6	1.6	105	8	ADO20991	Ado20991 PDZ domain
732	6	1.6	94	3	AAy87676	AAy87676 Feline hu	805	6	1.6	105	8	ADR2932	Adr2932 PDZ domain
733	6	1.6	94	4	AAO08266	AAO08266 Human pol	806	6	1.6	106	3	AAB62915	AbB62915 Human sbg
734	6	1.6	94	4	AAU41505	AAU41505 Propionib	807	6	1.6	106	4	AAU67382	Aau67382 Propionib
735	6	1.6	94	4	AAU49337	AAU49337 Propionib	808	6	1.6	106	4	ABM63901	Abm63901 Propionib
736	6	1.6	94	5	ABP43800	ABP43800 Breast an	809	6	1.6	106	8	ADR08625	Adr08625 Human pro
737	6	1.6	94	5	ADK35549	ADK35549 Novel hum	810	6	1.6	107	3	AAg15104	Aag15104 Arabidops
738	6	1.6	94	6	ABM38024	ABM38024 Propionib	811	6	1.6	107	4	AAO11955	Aao11955 Human pol
739	6	1.6	94	6	ABM45856	ABM45856 Propionib	812	6	1.6	107	4	AAU67658	Aau67658 Propionib
740	6	1.6	94	8	ADP29249	ADP29249 Human sec	813	6	1.6	107	4	AAU43341	Aau43341 Propionib
741	6	1.6	95	4	AAO09840	AAO09840 Human pol	814	6	1.6	107	5	ABB49473	Abb49473 Listeria
742	6	1.6	95	4	AAO12881	AAO12881 Human pol	815	6	1.6	107	6	ABM64177	Abm64177 Propionib
743	6	1.6	95	5	ADJ33675	ADJ33675 Protein o	816	6	1.6	107	6	ABM39860	Abm39860 Propionib
744	6	1.6	95	6	ABR40600	ABR40600 Typha lat	817	6	1.6	107	7	ABU40771	Abu40771 Protein e
745	6	1.6	95	7	ADC23499	ADC23499 Polypepti	818	6	1.6	108	2	ADH62496	Adh62496 Cat aller
746	6	1.6	97	2	AAr12123	AAr12123 TRFP chai	819	6	1.6	108	2	AAy29254	Aay29254 Amino aci
747	6	1.6	97	3	AAy51472	AAy51472 Human TRF	820	6	1.6	108	3	AAy64592	Aay64592 Nonclassi
748	6	1.6	97	3	AAb28935	AAb28935 T cell re	821	6	1.6	108	4	AAm92134	Aam92134 Human dig
749	6	1.6	97	3	AAy90105	AAy90105 Cat TRFP	822	6	1.6	108	7	ABO79817	Abo79817 Pseudomon
750	6	1.6	97	3	AAy87675	AAy87675 Feline hu	823	6	1.6	109	2	AAr12122	Aar12122 TRFP I ch
751	6	1.6	97	4	ABB11488	ABB11488 Human bA2	824	6	1.6	109	2	AAr41985	Aar41985 Human T c
752	6	1.6	97	4	ABG01986	ABG01986 Novel hum	825	6	1.6	109	2	AAy36541	Aay36541 TRFP chai
753	6	1.6	97	5	ABP64141	ABP64141 Human ORF	826	6	1.6	109	2	AAy25593	Aay25593 Felis sp.
754	6	1.6	97	5	ABP32075	ABP32075 Human ORF	827	6	1.6	109	3	AAy51471	Aay51471 Human TRF
755	6	1.6	97	5	ABP31898	ABP31898 Human ORF	828	6	1.6	109	3	AAb28934	Aab28934 T cell re

829	6	1.6	109	3	AAV90104	Aav90104	Cat TRFP	902	6	1.6	121	4	AAM58441	Aam58441	Human bra
830	6	1.6	109	3	AAV87674	Aav87674	Feline hu	903	6	1.6	121	4	ABG52650	Abg52650	Human liv
831	6	1.6	109	3	AAV10814	Aav10814	Arabidops	904	6	1.6	121	4	ABB16886	Abb16886	Human ner
832	6	1.6	109	3	AAAG2631	Aag2631	Arabidops	905	6	1.6	121	5	ADK37031	Adk37031	Novel hum
833	6	1.6	109	4	AAU20654	Aau20654	Human sec	906	6	1.6	121	7	ADF06894	Adf06894	Bacterial
834	6	1.6	109	4	AAAM90465	Aam90465	Human imm	907	6	1.6	121	8	ADR10706	Adr10706	P439-End
835	6	1.6	109	7	ADC34843	Adc34843	Cat aller	908	6	1.6	122	3	AAAG09288	Aag09288	Arabidops
836	6	1.6	109	8	ADM12179	Adm12179	Cat aller	909	6	1.6	122	3	AAAG08662	Aag08662	Human EST
837	6	1.6	110	2	AAAR27370	Aar27370	TRFP Chai	910	6	1.6	122	4	AAAM24405	Aam24405	Human EST
838	6	1.6	110	3	AAAG01697	Aag01697	Human sec	911	6	1.6	122	6	ABU39878	Abu39878	Protein e
839	6	1.6	110	4	AAAO05957	Aao05957	Human pol	912	6	1.6	122	8	ADM87772	Adm87772	Human EST
840	6	1.6	110	4	ABB16303	Abb16303	Human ner	913	6	1.6	122	8	ADN174035	Adn174035	Thale cre
841	6	1.6	110	7	ADFI13888	Adfi13888	Human end	914	6	1.6	123	2	AAAR14620	Aar14620	Protein e
842	6	1.6	111	2	AAAR12121	Aar12121	TRFP Chai	915	6	1.6	123	2	AAAR38784	Aar38784	HEV ORF3
843	6	1.6	111	2	AAAR27369	Aar27369	TRFP Chai	916	6	1.6	123	2	AAAR38786	Aar38786	HEV ORF3
844	6	1.6	111	3	AAAY51470	Aay51470	Human TRP	917	6	1.6	123	2	AAAR39307	Aar39307	Mexico st
845	6	1.6	111	3	AAAB28933	Aab28933	T cell re	918	6	1.6	123	2	AAAR39305	Aar39305	Burma str
846	6	1.6	111	3	AAAY90103	Aay90103	Cat TRFP	919	6	1.6	123	2	AAAR51266	Aar51266	HEV strai
847	6	1.6	111	3	AAAY87673	Aay87673	Feline hu	920	6	1.6	123	2	AAAR70324	Aar70324	Hepatitits
848	6	1.6	111	3	AAAG45731	Aag45731	Arabidops	921	6	1.6	123	2	AAAR96098	Aar96098	Hepatitits
849	6	1.6	111	3	AAAG27262	Aag27262	Zea mays	922	6	1.6	123	2	AAAR96097	Aar96097	Hepatitits
850	6	1.6	111	4	AAAB45791	Aab45791	Propionib	923	6	1.6	123	2	AAAR91815	Aar91815	Hepatitits
851	6	1.6	111	4	AAAB15350	Abb15350	Human ner	924	6	1.6	123	2	AAAW80198	Aaw80198	Protein e
852	6	1.6	111	5	ABJO5515	Abj05515	Human bre	925	6	1.6	123	2	AAAW81521	Aaw81521	Hepatitits
853	6	1.6	111	6	ABMA42310	Abm42310	Propionib	926	6	1.6	123	2	AAAW76370	Aaw76370	Hepatitits
854	6	1.6	111	8	ABO55419	Abo55419	Human gen	927	6	1.6	123	2	AAAW71211	Aaw71211	Protein e
855	6	1.6	112	3	AAAY91641	Aay91641	Human sec	928	6	1.6	123	2	AAAW93400	Aaw93400	Human HEV
856	6	1.6	112	3	AAAU17715	Aau17715	Novel hum	929	6	1.6	123	2	AAAW93401	Aaw93401	Human HEV
857	6	1.6	112	4	AAAB93399	Aab93399	Human pro	930	6	1.6	123	2	AAAW93399	Aaw93399	Human HEV
858	6	1.6	112	5	ABBO43339	Abb04339	Human sig	931	6	1.6	123	2	AAAW93404	Aaw93404	Human HEV
859	6	1.6	112	7	ADGA1095	Adg41095	Human res	932	6	1.6	123	2	AAAW93397	Aaw93397	Human HEV
860	6	1.6	112	7	ADMO5491	Adm05491	Human pro	933	6	1.6	123	2	AAAW93398	Aaw93398	Human HEV
861	6	1.6	112	7	ADIP96869	Adi96869	Human res	934	6	1.6	123	2	AAAW93402	Aaw93402	Human HEV
862	6	1.6	112	8	ADP29288	Adp29288	Human sec	935	6	1.6	123	2	AAAW93403	Aaw93403	Human HEV
863	6	1.6	113	2	AAAY36969	Aay36969	Amino aci	936	6	1.6	123	3	AAAB24121	Aab24121	Hepatitits
864	6	1.6	114	3	AAAG57187	Aag57187	Arabidops	937	6	1.6	123	4	AAAB62524	Aab62524	HEV-Burma
865	6	1.6	114	4	AAAB74692	Aab74692	Human pro	938	6	1.6	123	4	AAAU14521	Aau14521	Human nov
866	6	1.6	114	4	AAUA6546	Aua6546	Propionib	939	6	1.6	123	4	AAAU14521	Aau14521	Human nov
867	6	1.6	114	4	ABG12492	Abg12492	Novel hum	940	6	1.6	123	4	AAAO03859	Aao03859	Human pol
868	6	1.6	114	6	ABMA43065	Abm43065	Propionib	941	6	1.6	123	4	ADHI13472	Adh13472	Hepatitits
869	6	1.6	114	8	ADL71717	Adl71717	Novel hum	942	6	1.6	123	5	AAAO15700	Aao15700	Hepatitits
870	6	1.6	114	8	ADQ65348	Adq65348	Novel hum	943	6	1.6	123	5	ABAB1678	Abab1678	Hepatitits
871	6	1.6	115	2	AAAY85810	Aay85810	S. pneumo	944	6	1.6	123	6	ADAA50061	Ada50061	Hepatitits
872	6	1.6	115	4	AAAY66603	Aay66603	Propionib	945	6	1.6	123	6	ADAA50061	Ada50061	Hepatitits
873	6	1.6	115	6	ABU01115	Abu01115	S. pneumo	946	6	1.6	123	7	ADDA24377	Ada24377	Hepatitits
874	6	1.6	115	6	ABMG31122	Abm63122	Propionib	947	6	1.6	123	7	ADFI3887	Adfi3887	Human end
875	6	1.6	115	6	ADAA34066	Ada34066	Acinetoba	948	6	1.6	124	2	AAAW35829	Aaw35829	Hepatitits
876	6	1.6	115	8	ADK46297	Adk46297	Streptoco	949	6	1.6	124	2	AAAW35828	Aaw35828	Hepatitits
877	6	1.6	115	8	ADRA94868	Adr94868	Novel S.	950	6	1.6	124	3	AAAG57186	Aag57186	Arabidops
878	6	1.6	116	3	AAAB58883	Aab58883	Breast an	951	6	1.6	124	4	AAAO01658	Aao01658	Human pol
879	6	1.6	116	4	AAAB86824	Aab86824	Human pro	952	6	1.6	124	6	ABUA0960	Abua0960	Protein e
880	6	1.6	116	4	AAAB86827	Aab86827	Human pro	953	6	1.6	124	8	ADHA08339	Adha08339	Human pol
881	6	1.6	116	4	AAAO05007	Aao05007	Human pol	954	6	1.6	125	3	AAAG45730	Aag45730	Arabidops
882	6	1.6	116	5	ABBA49210	Abb49210	Listeria	955	6	1.6	125	4	AAAE01524	Aae01524	Human gen
883	6	1.6	117	4	ABG22221	Abg22221	Novel hum	956	6	1.6	125	6	ABG743350	Abg743350	Human Igb
884	6	1.6	118	3	AAAB62910	Aab62910	Human sbg	957	6	1.6	125	6	ABU71045	Abu71045	Human adi
885	6	1.6	118	4	ABAB65568	Abb65568	Drosophi	958	6	1.6	125	6	ABU71045	Abu71045	Human exp
886	6	1.6	118	4	AAAB68611	Aab68611	Human VAT	959	6	1.6	125	6	ABU04996	Abu04996	Human exp
887	6	1.6	118	4	AAAM39722	Aam39722	Human pol	960	6	1.6	125	6	ABU05002	Abu05002	Human exp
888	6	1.6	118	4	AAAU52176	Aau52176	Propionib	961	6	1.6	125	6	ABU05005	Abu05005	Human exp
889	6	1.6	118	4	AAU61896	Aau61896	Propionib	962	6	1.6	126	3	AAAB62912	Aab62912	Human sbg
890	6	1.6	118	5	ABG32647	Abg32647	Human vac	963	6	1.6	126	3	AAAB57221	Aab57221	Human rep
891	6	1.6	118	6	ABMA48695	Abm48695	Propionib	964	6	1.6	126	4	AAAM94733	Aam94733	Human pro
892	6	1.6	118	6	ABMA58415	Abm58415	Propionib	965	6	1.6	126	4	AAU22757	Aau22757	Human pro
893	6	1.6	118	8	ADG22297	Adg22297	Cyanophag	966	6	1.6	126	7	ADJO9330	Adjo9330	Human pro
894	6	1.6	119	3	AAAY75023	Aay75023	Neisseria	967	6	1.6	127	4	AAAB87621	Aab87621	Bovine ma
895	6	1.6	119	3	AAAG47785	Aag47785	Arabidops	968	6	1.6	127	4	AAAE09694	Aae09694	Human gen
896	6	1.6	119	3	AAAG11329	Aag11329	Arabidops	969	6	1.6	127	4	AAAM41139	Aam41139	Human pol
897	6	1.6	119	4	ABGI6822	Abgi6822	Novel hum	970	6	1.6	127	7	ADCC2072	Adc2072	Human pro
898	6	1.6	119	4	ABGI0294	Abgi0294	Novel hum	971	6	1.6	127	8	ABOS58976	Abos58976	Human gen
899	6	1.6	119	4	AAAG89199	Aag89199	Human sec	972	6	1.6	128	2	AAAY60397	Aay60397	Human nor
900	6	1.6	119	7	ADCC26972	Adc26972	Sorangium	973	6	1.6	128	4	AAAB86828	Aab86828	Human pro
901	6	1.6	120	3	AAAY95705	Aay95705	Cosmid cH	974	6	1.6	128	4	AAAB86825	Aab86825	Human pro

975	6	1.6	128	5	AA020562	Human clu
976	6	1.6	129	4	AAU86721	Novel hum
977	6	1.6	129	4	AAM41508	Human pol
978	6	1.6	129	5	AAU79828	Mouse typ
979	6	1.6	129	6	ADA32873	Acinetoba
980	6	1.6	129	7	ADB60055	Connectiv
981	6	1.6	130	4	ABB11294	Human leu
982	6	1.6	130	4	AA081275	Human app
983	6	1.6	130	4	AAM06482	Human foe
984	6	1.6	130	6	ABR47613	Breast ca
985	6	1.6	130	6	ABB99343	Amino aci
986	6	1.6	130	7	ABO74860	Pseudomon
987	6	1.6	131	4	AA025812	Human pro
988	6	1.6	131	6	ABM65276	Propionib
989	6	1.6	131	6	ABU54655	Human CAL
990	6	1.6	131	7	ADI60367	Secreted
991	6	1.6	131	7	ADI60368	Secreted
992	6	1.6	132	4	AG75552	Human col
993	6	1.6	132	4	AG70919	C albican
994	6	1.6	132	5	AAU75333	S. pombe
995	6	1.6	133	5	ABP08892	Human ORF
996	6	1.6	133	5	AAU75332	Yeast ICB
997	6	1.6	133	7	ABO74063	Pseudomon
998	6	1.6	134	5	ADK34378	Novel hum
999	6	1.6	135	3	AA084017	Amino aci
1000	6	1.6	135	4	ABG07643	Novel hum

ALIGNMENTS

RESULT 1	
AAB48007	
ID AAB48007 standard; protein; 384 AA.	
AC AAB48007;	
DT 19-MAR-2001 (first entry)	
DE Human sphingosine kinase protein sequence.	
EX	
KW Sphingosine kinase; antiarthritic; antiasthmatic; antiarteriosclerotic;	
KW antiinflammatory; neuroprotective; antibacterial; immunosuppressive;	
KW human.	
OS Homo sapiens.	
XX WO200070028-A1.	
XX	
PD 23-NOV-2000.	
XX	
PF 12-MAY-2000; 2000WO-AU000457.	
XX	
PR 13-MAY-1999; 99AU-00000339.	
PR 08-JUL-1999; 99AU-00001504.	
XX	
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.	
XX	
PI Pitson SM, Wattenberg BW, Xia P, D'andrea RJ, Gamble JR;	
PI Vadas MA;	
XX	
DR WPI; 2001-016227/02.	
DR N-PSDB; AAC84161.	
XX	
PT Novel sphingosine kinase protein and nucleic acid molecules for	
PT diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma,	
PT atherosclerosis, inflammation, meningitis, multiple sclerosis and septic	
PT shock.	
XX	
PS Claim 9; Fig 7a; 100pp; English.	
XX	
CC This represents a human sphingosine kinase (SK) protein. The human SK	
CC protein, encoding nucleic acids and modulators are useful for modulating	

CC	expression, functional activity or cellular functional activity of
CC	sphingosine kinase in a subject and also for treating a mammal by
CC	modulating the activity of SK. Diseases treated by regulating SK cellular
CC	activity include rheumatoid arthritis, asthma, atherosclerosis,
CC	inflammation, meningitis, multiple sclerosis and septic shock
XX	
SQ	Sequence 384 AA;
	Query Match 100.0%; Score 384; DB 4; Length 384;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MDPAGGPRGVLP RCRVLVLLNPRGGKQKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
Db	1 MDPAGGPRGVLP RCRVLVLLNPRGGKQKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
Qy	61 RELVRSBELGRWDALVVMGSDGLMHEVVGMLMRPDMETAIQKPLCSLPAGSGNALAASL 120
Db	61 RELVRSBELGRWDALVVMGSDGLMHEVVGMLMRPDMETAIQKPLCSLPAGSGNALAASL 120
Qy	121 NHYAGYEQVTNEDLLTNTCTLLCCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVLE 180
Db	121 NHYAGYEQVTNEDLLTNTCTLLCCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVLE 180
Qy	181 SEKYYRRLGEMRFTLTGTLRLAALTYGRLAYLPGVGVSKTSPASVWVOGQPDVDAHLVP 240
Db	181 SEKYYRRLGEMRFTLTGTLRLAALTYGRLAYLPGVGVSKTSPASVWVOGQPDVDAHLVP 240
Qy	241 LEEVPVSHWTVPDDEFVLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
Db	241 LEEVPVSHWTVPDDEFVLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
Qy	301 RLFLAMEKGRHMEYECPLYVVPVAFRLPDKGKGMFAVDGELMVSEAVQGVHPNYFW 360
Db	301 RLFLAMEKGRHMEYECPLYVVPVAFRLPDKGKGMFAVDGELMVSEAVQGVHPNYFW 360
Qy	361 MVSGCVPFPPSWKPDQMPPEEPL 384
Db	361 MVSGCVPFPPSWKPDQMPPEEPL 384
RESULT 2	
ADF28783	
ID ADF28783 standard; protein; 384 AA.	
XX	
AC ADF28783;	
XX	
DT 12-FEB-2004 (first entry)	
XX	
DE Human sphingosine kinase (hSK)1 protein sequence.	
XX	
KW SK; sphingosine kinase; phosphorylation; protein kinase; ERK1; ERK2;	
KW CDK2; cytosolic; antiinflammatory; immunosuppressive; antiarthritic;	
KW antiirheumatic; antiarteriosclerotic; antiasthmatic; human; hSK1; enzyme.	
XX	
OS Homo sapiens.	
XX	
PH	Key Location/Qualifiers
FT Modified-site 148	/note= "phosphorylated"
FT Modified-site 181	/note= "phosphorylated"
FT Modified-site 184	/note= "phosphorylated"
FT Modified-site 225	/note= "phosphorylated"
FT Modified-site 250	/note= "phosphorylated"
FT Modified-site 250	/note= "phosphorylated"
XX	
FN WO2003082322-A1.	
XX	
PD 09-OCT-2003.	
XX	

PF	28-MAR-2003; 2003WO-AU000388.	
XX		
PR	28-MAR-2002; 2002AU-00001448.	
PR	05-APR-2002; 2002AU-00001538.	
PR	08-APR-2002; 2002AU-00001621.	
PR	19-SEP-2002; 2002AU-00951668.	
PR	21-JAN-2003; 2003AU-00900230.	
XX		
PA	(MEDV-) MEDVET SCI PTY LTD.	
XX		
PI	Pitson SM, Xia P, Moretti PA, Verwey JR, Vadas MA, Wattenberg BW;	
XX		
XX	WPI; 2003-803967/75.	
XX		
PT	Modulating sphingosine kinase functional activity for treating arthritis,	
PT	atherosclerosis and asthma by contacting the sphingosine kinase with an	
PT	agent for a time and under conditions to modulate phosphorylation of the	
PT	kinase.	
XX		
PS	Example 2; SEQ ID NO 12; 95pp; English.	
XX		
CC	The invention relates to modulating sphingosine kinase (SK) functional	
CC	activity. The method involves contacting the SK with an agent for a time	
CC	and under conditions to modulate phosphorylation of the SK where inducing	
CC	or agonizing the phosphorylation upregulates the SK activity and	
CC	inhibiting or antagonizing the phosphorylation down regulates SK	
CC	activity. The modulation of the phosphorylation is modulation of proline-	
CC	directed protein kinase catalyzed phosphorylation. The proline-directed	
CC	kinase is ERK1, ERK2 or CDK2. The modulation is preferably down-	
CC	regulation. The methods and agents are useful for treating and/or	
CC	prophylaxis of a condition characterized by aberrant, unwanted or	
CC	inappropriate cellular activity or sphingosine kinase functional	
CC	activity, e.g. a neoplastic condition or an inflammatory condition such	
CC	as rheumatoid arthritis, atherosclerosis, asthma, autoimmune disease or	
CC	inflammatory bowel disease. The present sequence represents a human SK	
CC	(hSK)1 protein.	
XX		
SQ	Sequence 384 AA;	
Query Match 100.0%; Score 384; DB 7; Length 384;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MDPAGGPRGVLPPCRVLVLLNPRGGKQALQIFRSHVQPLLAERISFTLMLTERRNHA	60
Db		
Db	1 MDPAGGPRGVLPPCRVLVLLNPRGGKQALQIFRSHVQPLLAERISFTLMLTERRNHA	60
QY	61 RELVRSSEELGRWDALVMSGDGLMHVNVGLMERPDWETAIOKPLCSLPAGSGNALAASL	120
Db		
Db	61 RELVRSSEELGRWDALVMSGDGLMHVNVGLMERPDWETAIOKPLCSLPAGSGNALAASL	120
QY	121 NHVAGYEQVTNEDLLTNTCLLRCRLSPNLLSLHTASGLRFLSVLSLAWGFADVDLE	180
Db		
Db	121 NHVAGYEQVTNEDLLTNTCLLRCRLSPNLLSLHTASGLRFLSVLSLAWGFADVDLE	180
QY	181 SEKYRRLGEMRFTLGTFLRLAALTRYRLAYLIPVGRVSGKTPASPVVVOGGPVDAHLVP	240
Db		
Db	181 SEKYRRLGEMRFTLGTFLRLAALTRYRLAYLIPVGRVSGKTPASPVVVOGGPVDAHLVP	240
QY	241 LEEPVRSHWTVVDEDPVLVLLHSLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAML	300
Db		
Db	241 LEEPVRSHWTVVDEDPVLVLLHSLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAML	300
QY	301 RLFLAMEKGRHMEYECFYLVPVPAFLRLEPKDGKMFADVGBELMWSEAVQGVHPNFW	360
Db		
Db	301 RLFLAMEKGRHMEYECFYLVPVPAFLRLEPKDGKMFADVGBELMWSEAVQGVHPNFW	360
QY	361 MVSCGVEPPPSWKPQQMPPEEPL	384
Db		
Db	361 MVSCGVEPPPSWKPQQMPPEEPL	384
RESULT 3		

AA18659	
ID	AA18659 standard; protein; 384 AA.
XX	
AC	AA18659;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	A human regulator of intracellular phosphorylation.
XX	
KW	Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
KW	neurological disorder; Parkinson's disease; demyelinating disease;
KW	meningitis; developmental disorder; neuromuscular disorder; cancer;
KW	myasthenia gravis; cell proliferative disorder; actinic keratosis;
KW	arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis;
KW	autoimmune disorder; inflammatory disorder; Addison's disease;
KW	acquired immunodeficiency disease; allergy; diabetes mellitus;
KW	rheumatoid arthritis; microbial infection; trauma.
OS	Homo sapiens.
XX	
XX	
PH	Key
FT	Active-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
XX	WO200055332-A2.
XX	
PD	21-SEP-2000.
XX	
PF	17-MAR-2000; 200WO-US007277.
XX	
PR	18-MAR-1999; 99US-0125593P.
PR	20-MAY-1999; 99US-0135049P.
PR	09-JUL-1999; 99US-0143188P.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Bandman O, Tang YT, Yue H, Hillman JL, Baughn MR, Azimzai Y;
PI	Lu DAM, Au-Young J;
XX	
DR	WPI; 2000-602121/57.
DR	N-PSDB; AAA75676.
XX	
PT	Novel human intracellular phosphorylation regulator polypeptides and
PT	polynucleotides for diagnosis, prevention and treatment of neurological,
PT	cell proliferative and autoimmune/inflammatory disorders.
XX	
PS	Claim 1; Page 77-78; 96pp; English.
XX	
CC	The present sequence represents a human regulator of intracellular
CC	phosphorylation (HRIP). HRIP is useful for screening agonists and
CC	antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are
CC	useful for treating a disease or condition associated with decreased or
CC	increased expression of functional HRIP. Diseases treated or diagnosed
CC	include neurological disorders such as stroke, Parkinson's disease,
CC	demyelinating diseases, bacterial and viral meningitis and other
CC	developmental disorders of the central nervous system, neuromuscular
CC	disorders, myasthenia gravis, cell proliferative disorders such as
CC	actinic keratosis, arteriosclerosis, atherosclerosis and cancer including
CC	leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder,
CC	bone, bone marrow, liver, lung, muscle, ovary, autoimmune/inflammatory
CC	disorder such as Addison's disease, acquired immunodeficiency diseases,

```
CC allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial
CC infection and trauma
XX
SQ Sequence 384 AA;
Query Match      87.5%; Score 336; DB 3; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTLMLTERRNHA 60
Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTLMLTERRNHA 60
Qy 61 RELVRSBELGRWDALVWMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVRSBELGRWDALVWMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Qy 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAWGFIADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAWGFIADVDLE 180
Qy 181 SEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVQQGPVDHLVP 240
Db 181 SEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVQQGPVDHLVP 240
Qy 241 LEEPVPSSHWTVPDDEFVLVLALLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPSSHWTVPDDEFVLVLALLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGK 336
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGK 336
RESULT 4
ID AAB94589
XX AAB94589 standard; protein; 384 AA.
AC AAB94589;
XX
XX 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15394.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 09-JUN-2000; 2000JP-00183767.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 15394; 2537pp + Sequence Listing; English.
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XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 384 AA;
Query Match      87.5%; Score 336; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTLMLTERRNHA 60
Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTLMLTERRNHA 60
Qy 61 RELVRSBELGRWDALVWMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVRSBELGRWDALVWMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Qy 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAWGFIADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAWGFIADVDLE 180
Qy 181 SEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVQQGPVDHLVP 240
Db 181 SEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVQQGPVDHLVP 240
Qy 241 LEEPVPSSHWTVPDDEFVLVLALLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPSSHWTVPDDEFVLVLALLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGK 336
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGK 336
RESULT 5
AAB93955
ID AAB93955 standard; protein; 384 AA.
XX
XX AAB93955;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:13997.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
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PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
PA
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
XX Claim 8; SEQ ID NO 13997; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
XX
XX Sequence 384 AA;
SQ
Query Match 87.5%; Score 336; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPAGGPRGVLPKPCRVLLNPRGGKALQLFRSHVQPLLAEBISFTLMLTERRNHA 60
DB 1 MDPAGGPRGVLPKPCRVLLNPRGGKALQLFRSHVQPLLAEBISFTLMLTERRNHA 60
QY 61 RELVRSEELGRWDALVVMGSDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
DB 61 RELVRSEELGRWDALVVMGSDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
QY 121 NHVAYEQVTNEDLLTCTLLCRRLLSPNNLLSLHTAGSLRFLSVLSLAWGFADVDLE 180
DB 121 NHVAYEQVTNEDLLTCTLLCRRLLSPNNLLSLHTAGSLRFLSVLSLAWGFADVDLE 180
QY 181 SEKRYRLGENRFTLTGTLFLRLAALTYRGLAYLPVGRVSGKTPASPVPVQQGPVDAHLVP 240
DB 181 SEKRYRLGENRFTLTGTLFLRLAALTYRGLAYLPVGRVSGKTPASPVPVQQGPVDAHLVP 240
QY 241 LEEFPVSHWTVPDEDFVLVLALLHSLGSEMPAAMPGRCAAGVMHLFYVRAGVSAMLL 300
DB 241 LEEFPVSHWTVPDEDFVLVLALLHSLGSEMPAAMPGRCAAGVMHLFYVRAGVSAMLL 300
QY 301 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPEKDGK 336
|||||

DB 301 RLFLAMEKGRHMEYECPLYVYVVPVAFRLPEKDGK 336
RESULT 6
AAE00924
ID AAE00924 standard; protein; 384 AA.
XX
XX AAE00924;
XX
XX 04-JUL-2001 (first entry)
XX Human sphingosine kinase type 1 (hsk1).
XX
XX Human; sphingosine kinase type 1; skl; chromosome 17q25.2;
KW sphingosine-1-phosphate; SIP; drug screening; therapy; haemostasis;
KW thrombosis; allergic reaction; proliferative disease; cancer;
KW haematopoietic disorder; leukaemia; cardiovascular disease; stroke;
KW atherosclerosis; coronary artery disease; dyslipidaemia; diabetes;
KW autoimmune disease; inflammatory disease; multiple sclerosis;
KW T helper-1 related disease; chronic obstructive pulmonary disease;
KW asthma; myocardial infarction; neurodegenerative disorder; wound healing;
KW embryogenesis; anticoagulant; neuroprotective; neuroprotective;
KW antipsoriatic; antiarthritic; cytostatic; cardiant; vulnerary.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
FT Region 16..95
FT /label= Conserved_region
XX
XX WO200131029-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-EP009498.
XX
XX 28-OCT-1999; 99US-0162307P.
XX 07-FEB-2000; 2000US-0180525P.
XX (WARN) WARNER LAMBERT CO.
XX
XX Allen J, Gosink M, Melendez AJ, Takacs L;
XX
XX WPI; 2001-300510/31.
XX N-PSDB; AAD04477.
XX
XX New human sphingosine kinase type I gene for screening drug candidates particularly inhibitors used for preventing or treating e.g. atherosclerosis, thrombosis, asthma and diabetes.
XX
XX Claim 3; Fig 1; 91pp; English.
XX
XX The present sequence is human sphingosine kinase type 1 (hsk1). The hsk1 gene is located on chromosome 17q25.2. The skl converts the substrate sphingosine to sphingosine-1-phosphate (SIP). The skl gene and encoded polypeptide are applicable in screening drug candidates particularly inhibitors for preventing or treating disorders such as haemostasis, thrombosis, allergic reactions, proliferative diseases including cancer, haematopoietic disorders such as leukaemia, cardiovascular diseases such as stroke, atherosclerosis and coronary artery disease, dyslipidaemia, diabetes including type I and type II diabetes, autoimmune and inflammatory diseases such as multiple sclerosis, T helper-1 related diseases, chronic obstructive pulmonary disease, asthma, myocardial infarction, neurodegenerative disorders, natural wound healing processes and embryogenesis
XX
XX Sequence 384 AA;
Query Match 87.5%; Score 336; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPAGGPRGVLPKPCRVLLNPRGGKALQLFRSHVQPLLAEBISFTLMLTERRNHA 60

|||||
1 MDPAGGPRGVLP R P C R V L I L N P R G G K G K A L Q L F R S H V Q P L L A B A E I S F T I M L T E R R N H A 60
61 RELVRSBELGRWDALVVMG D G L M H E V V N G L M E R P D M E T A I Q K P L C S L P A G S G N A L A A S L 120
61 RELVRSBELGRWDALVVMG D G L M H E V V N G L M E R P D M E T A I Q K P L C S L P A G S G N A L A A S L 120
121 N H Y A G Y E Q V T N E D L L T N C T L L C R R L L S P M N L L S H T A S G L R L F S V L S L A W G F T A D V D L E 180
121 N H Y A G Y E Q V T N E D L L T N C T L L C R R L L S P M N L L S H T A S G L R L F S V L S L A W G F T A D V D L E 180
181 S E K Y R R L G E M R F T L G T F L R L A A L R T Y R G R L A Y L P V G R V G S K T P A S P V V V Q Q G P V D A H L V P 240
181 S E K Y R R L G E M R F T L G T F L R L A A L R T Y R G R L A Y L P V G R V G S K T P A S P V V V Q Q G P V D A H L V P 240
241 L E E P V P S H W T V V P D E D F V L V L A L L H S L G S E M F A P M G R C A A G V M H L F Y Y R A G V S R A M L L 300
241 L E E P V P S H W T V V P D E D F V L V L A L L H S L G S E M F A P M G R C A A G V M H L F Y Y R A G V S R A M L L 300
301 R L F L A M E K G R H M E Y E C P Y L V V P V V A F R L E P K D G K G 336
301 R L F L A M E K G R H M E Y E C P Y L V V P V V A F R L E P K D G K G 336

RESULT 7

ABG31586
ID ABG31586 standard; protein; 384 AA.

AC ABG31586;

DT 05-NOV-2002 (first entry)

DE Human sphingosine kinase 1 (SPHK1).

Human; sphingosine kinase 1; SPHK1; blood vessel formation; primate;
congestive heart failure; myocardial ischaemia; wound healing;
ischaemia-reperfusion injury; peripheral arterial disease; angiogenesis;
coronary artery disease; peripheral vascular disease; fracture repair;
reconstructive surgery; transplantation; islet transplant; tendon repair;
sports injury; ulcer; thromboangitis obliterans; Buerger's disease;
periodontal tissue regeneration; radiotherapy-induced oesophagitis.

OS Homo sapiens.

PN WO200228406-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-EP011513.

PR 05-OCT-2000; 2000US-0238230P.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Liao G, Stefansson S, Su J;

DR WPI; 2002-608171/65.

DR N-PSDB; ABK90198.

Inducing blood vessel formation, or preventing/treating congestive heart failure, ischemia-reperfusion injury, myocardial ischemia and peripheral arterial diseases in animal, by administering sphingosine kinase.

PS Disclosure; Page 35-36; 45pp; English.

CC The present invention relates to a new method of inducing blood vessel formation in an animal. The method of the invention involves administering sphingosine kinase to the animal. The method is useful for inducing blood vessel formation in an animal, or preventing or treating congestive heart failure, myocardial ischaemia, ischaemia-reperfusion injury and peripheral arterial diseases in an animal, e.g. mammal (such as primate including human). The invention is also useful for treating

CC diseases or disorders selected from coronary artery disease, peripheral
CC vascular disease, wound healing and fracture repair, reconstructive
CC surgery, transplantation such as islet transplants, tendon repair/sports
CC injury, healing of ulcers, thromboangitis obliterans (Buerger's disease),
CC periodontal tissue regeneration and radiotherapy-induced oesophagitis.
CC The present amino acid sequence represents the human sphingosine kinase 1
CC (SPHK1) protein as described in the invention

XX SQ Sequence 384 AA;

Query Match 87.5%; Score 336; DB 5; Length 384;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAGGPRGVLP R P C R V L I L N P R G G K G K A L Q L F R S H V Q P L L A B A E I S F T I M L T E R R N H A 60

Db 1 MDPAGGPRGVLP R P C R V L I L N P R G G K G K A L Q L F R S H V Q P L L A B A E I S F T I M L T E R R N H A 60

Qy 61 RELVRSBELGRWDALVVMG D G L M H E V V N G L M E R P D M E T A I Q K P L C S L P A G S G N A L A A S L 120

Db 61 RELVRSBELGRWDALVVMG D G L M H E V V N G L M E R P D M E T A I Q K P L C S L P A G S G N A L A A S L 120

Qy 121 N H Y A G Y E Q V T N E D L L T N C T L L C R R L L S P M N L L S H T A S G L R L F S V L S L A W G F T A D V D L E 180

Db 121 N H Y A G Y E Q V T N E D L L T N C T L L C R R L L S P M N L L S H T A S G L R L F S V L S L A W G F T A D V D L E 180

Qy 181 S E K Y R R L G E M R F T L G T F L R L A A L R T Y R G R L A Y L P V G R V G S K T P A S P V V V Q Q G P V D A H L V P 240

Db 181 S E K Y R R L G E M R F T L G T F L R L A A L R T Y R G R L A Y L P V G R V G S K T P A S P V V V Q Q G P V D A H L V P 240

Qy 241 L E E P V P S H W T V V P D E D F V L V L A L L H S L G S E M F A P M G R C A A G V M H L F Y Y R A G V S R A M L L 300

Db 241 L E E P V P S H W T V V P D E D F V L V L A L L H S L G S E M F A P M G R C A A G V M H L F Y Y R A G V S R A M L L 300

Qy 301 R L F L A M E K G R H M E Y E C P Y L V V P V V A F R L E P K D G K G 336

Db 301 R L F L A M E K G R H M E Y E C P Y L V V P V V A F R L E P K D G K G 336

RESULT 8

ADE38365

ID ADE38365 standard; protein; 384 AA.

AC ADE38365;

DT 29-JAN-2004 (first entry)

DE Human protein 49863 amino acid sequence.

Human; tumorigenic disorder; angiogenic disorder; aberrant gene expression;
aberrant protein activity; cytostatic; antithyroid; antidiabetic;
ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
prostatic cancer; Grave's disease; diabetic retinopathy; protein 49863.

OS Homo sapiens.

PN WO2003065006-A2.

PD 07-AUG-2003.

PF 30-JAN-2003; 2003WO-US002588.

PR 31-JAN-2002; 2002US-0353600P.

PR 15-MAR-2002; 2002US-0364517P.

PR 09-APR-2002; 2002US-0371075P.

PR 10-APR-2002; 2002US-0371507P.

PR 16-APR-2002; 2002US-0372984P.

PR 19-APR-2002; 2002US-0374194P.

PR 24-MAY-2002; 2002US-0382995P.

PR 31-MAY-2002; 2002US-0385023P.

PR 14-JUN-2002; 2002US-0388853P.

PR 17-JUN-2002; 2002US-0389395P.

PR 25-JUN-2002; 2002US-0391324P.

Db 78 VRSEELGRWDALVVMGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY 137
QY 124 AGYEQVTHNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVLSLAWGFIADVDLSEK 183
Db 138 AGYEQVTHNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVLSLAWGFIADVDLSEK 197
QY 184 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOGPPVDAHLVPLEE 243
Db 198 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOGPPVDAHLVPLEE 257
QY 244 PVPSTHTVVPDDEDFVLVLALLSHLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAMLRLF 303
Db 258 PVPSTHTVVPDDEDFVLVLALLSHLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAMLRLF 317
QY 304 LAMEKGRHMEYECPLYVVPVFAFLRLEPKDGGK 336
Db 318 LAMEKGRHMEYECPLYVVPVFAFLRLEPKDGGK 350

RESULT 10
ADJ75387
ID ADJ75387 standard; protein; 398 AA.
AC ADJ75387;
DT 20-MAY-2004 (first entry)
DE Marker gene related amino acid sequence SEQ ID NO:639.
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
OS Homo sapiens.
XX
XX
XX EP1394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuvara K;
XX
XX WPI; 2004-193155/19.
XX
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX
XX Example 11; SEQ ID NO 639; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.

XX
SQ Sequence 398 AA;
Query Match 86.7%; Score 333; DB 8; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.6e-317;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGGPRGVLPRPCRVLLNPRGGKQALQFRSHVQPLLAEEISFTMLTERNHAREL 63
Db 18 AGGPRGVLPRPCRVLLNPRGGKQALQFRSHVQPLLAEEISFTMLTERNHAREL 77
QY 64 VRSEELGRWDALVVMGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY 123
Db 78 VRSEELGRWDALVVMGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY 137
QY 124 AGYEQVTHNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVLSLAWGFIADVDLSEK 183
Db 138 AGYEQVTHNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVLSLAWGFIADVDLSEK 197
QY 184 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOGPPVDAHLVPLEE 243
Db 198 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOGPPVDAHLVPLEE 257
QY 244 PVPSTHTVVPDDEDFVLVLALLSHLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAMLRLF 303
Db 258 PVPSTHTVVPDDEDFVLVLALLSHLHSGEMFAAPMGRCAAGVMHLFYVRAGVSRAMLRLF 317
QY 304 LAMEKGRHMEYECPLYVVPVFAFLRLEPKDGGK 336
Db 318 LAMEKGRHMEYECPLYVVPVFAFLRLEPKDGGK 350

RESULT 11
ADO22417
ID ADO22417 standard; protein; 398 AA.
XX
XX ADO22417;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human sphingosine kinase 1 (SPHK1).
XX
XX cytosolic; gene therapy; vaccine; SPHK1; EDG4; EDG5; EDG8; tumour;
XX cancer; pre-cancerous growth; colon cancer; ovarian cancer; lung cancer;
XX breast cancer; brain cancer; bladder cancer; liver cancer; kidney cancer;
XX head and neck cancer; stomach cancer; oesophagus cancer; human;
XX sphingosine kinase 1; enzyme.
XX
XX Homo sapiens.
XX
XX WO2004046332-A2.
XX
XX 03-JUN-2004.
XX
XX 18-NOV-2003; 2003WO-US036752.
XX
XX 19-NOV-2002; 2002US-0427202P.
XX 19-DEC-2002; 2002US-0434434P.
XX
XX (TULA-) TULARIK INC.

XX Li J, Powers S, Sin WC, Yang J;
XX WPI; 2004-420621/39.
XX N-PSDB; ADO22416, ADO22418.
XX
XX Use of SPHK1, EDG4, EDG5, and EDG8 genes for diagnosing, treating, or
XX preventing tumors and cancers in mammals, e.g. colon cancer, ovarian
XX cancer, lung cancer, breast cancer, brain cancer, bladder cancer, or
XX liver cancer.
XX
XX Disclosure; SEQ ID NO 2; 176pp; English.
XX
XX The invention describes SPHK1, EDG4, EDG5, and EDG8 genes for diagnosing,
XX treating, or preventing tumors and cancers in mammals. Also described
XX are: diagnosing a cancer in a mammal; inhibiting cancer or pre-cancerous
XX growth in a mammalian tissue; administering siRNA to a patient in need;
XX blocking in vivo expression of a gene; screening a test molecule for
XX SPHK1, EDG4, EDG5, or EDG8 antagonist activity; determining whether a
XX test molecule has SPHK1, EDG4, EDG5, or EDG8 antagonist activity;
XX determining the efficacy of a therapeutic treatment regimen in a patient;
XX selecting test molecules having a therapeutic effect in a patient;
XX treating cancer or pre-cancerous growth in a mammalian tissue; agonists
XX and inhibitors of SPHK1, EDG4, EDG5, or EDG8; antibodies which
XX specifically binds to SPHK1, EDG4, EDG5, or EDG8; and a pharmaceutical
XX composition comprising the antibodies. The SPHK1, EDG4, EDG5, or EDG8
XX genes are useful for diagnosing, treating, or preventing tumors and
XX cancers in mammals. Cancer includes colon cancer, ovarian cancer, lung
XX cancer, breast cancer, brain cancer, bladder cancer, liver cancer, kidney
XX cancer, head and neck cancer, stomach cancer, or esophagus cancer. They
XX can also be used as cancer vaccines. This is the amino acid sequence of
XX human sphingosine kinase 1 (SPHK1).
XX
XX Sequence 398 AA;
SQ
Query Match 86.7%; Score 333; DB 8; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.6e-317;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGGPRGLPRPCRVLLNPRGGKQALQFRSHVQPLLAEBISFTLMTERRNHAREL 63
DB 18 AGGPRGLPRPCRVLLNPRGGKQALQFRSHVQPLLAEBISFTLMTERRNHAREL 77
QY 64 VRSEELGRWDALVMSGDGLMHEVNVGLMERPDWETAIOKPLCSLPAGSGNALAASLNHY 123
DB 78 VRSEELGRWDALVMSGDGLMHEVNVGLMERPDWETAIOKPLCSLPAGSGNALAASLNHY 137
QY 124 AGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLISLAWGFADVDLESEK 183
DB 138 AGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLISLAWGFADVDLESEK 197
QY 184 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASPVVQQGPVD AHLVPLEE 243
DB 198 YRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASPVVQQGPVD AHLVPLEE 257
QY 244 PVPSTWTVDPEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFVVRAGVSRAMLRLRF 303
DB 258 PVPSTWTVDPEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFVVRAGVSRAMLRLRF 317
QY 304 LAMEKGRHMEYECPYLVVVPVAFRLPKDGGK 336
DB 318 LAMEKGRHMEYECPYLVVVPVAFRLPKDGGK 350
RESULT 12
ABR2391
ID ABR2391 standard; protein; 368 AA.
XX ABR2391;
XX AC
XX AC
XX AC
XX 06-NOV-2003 (first entry)
XX Human sphingosine kinase (SK) partial fragment.
DE

XX Sphingolipid; cytostatic; gene therapy; cancer; sphingolipidase; SPL;
XX sphingosine-1-phosphate lyase; sphingosine kinase; SK; enzyme; human.
XX
XX Homo sapiens.
XX
XX WO2003062390-A2.
XX
XX 31-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-US001739.
XX
XX 17-JAN-2002; 2002US-00053510.
XX
XX 17-JAN-2002; 2002US-0349582P.
XX
XX (CHIL-) CHILDRENS HOSPITAL & RES CENT AT OAKLAND.
XX
XX Saba JD, Fyrst H;
XX
XX WPI; 2003-663394/62.
XX
XX N-PSDB; ACF35857.
XX
XX Identifying an agent that modulates sphingolipid metabolism for treating
XX e.g., breast cancer by culturing a homozygous null mutant *Drosophila*
XX melanogaster in the absence and presence of a candidate agent.
XX
XX Disclosure; Page 125-126; 93pp; English.
XX
XX The invention relates to identifying an agent that modulates sphingolipid
XX metabolism. The method is useful for identifying an agent that modulates
XX sphingolipid metabolism for preparing a composition for treating a
XX disease associated with altered sphingolipid metabolism in a patient,
XX e.g., colon cancer, breast cancer, uterine cancer, stomach cancer,
XX ovarian cancer, lung cancer, kidney cancer, adenocarcinoma of the rectum
XX or hereditary sensory neuropathy type 1 or any one of the
XX sphingolipidases. The present sequence represents a human sphingosine
XX kinase (SK) partial fragment
XX
XX Sequence 368 AA;
SQ
Query Match 83.3%; Score 320; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.3e-304;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 VLVTANPRGGKQALQFRSHVQPLLAEBISFTLMTERRNHARELVRSEELGRWDALV 76
DB 1 VLVTANPRGGKQALQFRSHVQPLLAEBISFTLMTERRNHARELVRSEELGRWDALV 60
QY 77 VMSGDGLMHEVNVGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
DB 61 VMSGDGLMHEVNVGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120
QY 137 NCTLLCRLLSPMNLISLHTASGLRFSVLISLAWGFADVDLESEK YRRLGEMRFTLGT 196
DB 121 NCTLLCRLLSPMNLISLHTASGLRFSVLISLAWGFADVDLESEK YRRLGEMRFTLGT 180
QY 197 FLRLAALRTYRGLAYLPVGRVSKTPASPVVQQGPVD AHLVPLEE PVPSTWTVDPED 256
DB 181 FLRLAALRTYRGLAYLPVGRVSKTPASPVVQQGPVD AHLVPLEE PVPSTWTVDPED 240
QY 257 FVLVLLHSHLGSEMFAPMGRCAAGVMHLFVVRAGVSRAMLRLFLAMEKGRHMEYEC 316
DB 241 FVLVLLHSHLGSEMFAPMGRCAAGVMHLFVVRAGVSRAMLRLFLAMEKGRHMEYEC 300
QY 317 PYLVVVPVAFRLPKDGGK 336
DB 301 PYLVVVPVAFRLPKDGGK 320
RESULT 13
ABP71054
ID ABP71054 standard; protein; 384 AA.
XX

AC ABP71054;
 DT 14-APR-2003 (first entry)
 XX Human sphingosine kinase.
 DE TNF; tumour necrosis factor; sphingosine kinase; TRAF; TRAF2; cytostatic;
 KW TNF receptor-associated factor; antiinflammatory; antirheumatic; human;
 KW antiarthritic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 354
 FT /note= "Xaa is unknown"
 FT 379. .382
 FT /note= "specifically claimed peptide"
 XX
 XX WO200298458-A1.
 XX 12-DEC-2002.
 PD 03-JUN-2002; 2002WO-AU000710.
 XX 07-JUN-2001; 2001AU-00005521.
 PR 13-AUG-2001; 2001AU-00006978.
 PR 27-DEC-2001; 2001AU-00009759.
 XX (MEDV-) MEDVET SCI PTY LTD.
 PA Xia P, Wang L, Vadas M, Gamble J, Moretti P, Pitson S;
 PI WPI; 2003-201282/19.
 DR Modulating cytokine- or tumor necrosis factor-induced cellular activity,
 XX useful for treating or preventing a neoplastic condition, comprises
 PT modulating an intracellular sphingosine kinase-dependent signaling
 PT mechanism.
 XX Claim 8; Fig 9; 96pp; English.
 PS The invention relates to modulating cytokine-induced or tumour necrosis
 CC factor (TNF)-induced cellular activity. The method involves contacting
 CC the cell with an agent under conditions sufficient to modulate the
 CC interaction of sphingosine kinase with a TNF receptor-associated factor
 CC (TRAF), preferably TRAF2, where inducing the association up-regulates
 CC cellular activity, and inhibiting the association down-regulates cellular
 CC activity. The agent is useful for manufacturing a medicament for treating
 CC a mammal with a condition of aberrant, unwanted or inappropriate cytokine
 CC -induced or TNF-induced cellular activity. The methods are useful for
 CC modulating cytokine-induced or TNF-induced cellular activity, or for
 CC treating or preventing a condition of aberrant, unwanted or inappropriate
 CC cytokine-induced or TNF-induced cellular activity in a mammal, such as
 CC neoplastic condition or inflammation (e.g. rheumatoid arthritis). The
 CC present sequence represents a human sphingosine kinase
 XX Sequence 384 AA;
 SQ
 Query Match 74.7%; Score 287; DB 6; Length 384;
 Best Local Similarity 100.0%; Pred. No. 3.1e-272;
 Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPAGGPRGVLPFCRVLLVLPNPGGKGKALQFRSHVQPLLAABEISFTLMLTERNHA 60
 DB 1 MDPAGGPRGVLPFCRVLLVLPNPGGKGKALQFRSHVQPLLAABEISFTLMLTERNHA 60
 QY 61 RELVRSBELGRWDALVWMSGDGLMHEVVVNGLMERPDMETATQKPLCSLPAGSGNALAASL 120
 DB 61 RELVRSBELGRWDALVWMSGDGLMHEVVVNGLMERPDMETATQKPLCSLPAGSGNALAASL 120
 QY 121 NHYAGYEQVTTNEDLLTNCTLLCRLLSPMNLISHTASGLRFLSVLSLAWGFTIADVDLE 180
 DB 121 NHYAGYEQVTTNEDLLTNCTLLCRLLSPMNLISHTASGLRFLSVLSLAWGFTIADVDLE 180

QY 181 SEKYYRLGEMRFTLTGTLRLAALTYRGLAYLPVGRVSGSKTPASPVVVOGQPVDAHLVP 240
 DB 181 SEKYYRLGEMRFTLTGTLRLAALTYRGLAYLPVGRVSGSKTPASPVVVOGQPVDAHLVP 240
 QY 241 LEEVPVSHWTVVPDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHL 287
 DB 241 LEEVPVSHWTVVPDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHL 287
 RESULT 14
 ABB90209
 ID ABB90209 standard; protein; 333 AA.
 XX
 AC ABB90209;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2585.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX Homo sapiens.
 OS WO200190304-A2.
 XX
 PN 29-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-US016450.
 PF
 XX 19-MAY-2000; 2000US-0205515P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Birse CE, Rosen CA;
 XX WPI; 2002-122018/16.
 DR N-PSDB; ABL90618.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX Claim 11; SEQ ID NO 2585; 2081pp + Sequence Listing; English.
 PS The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at fip.wipo.int/pub/published_pct_sequences
 XX Sequence 333 AA;
 SQ
 Query Match 74.2%; Score 285; DB 5; Length 333;
 Best Local Similarity 100.0%; Pred. No. 2.4e-270;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2005, 11:52:56 ; Search time 41 Seconds
(without alignments)
901.152 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 2017
Sequence: 1 MDPAGRGVLPKPCRLVL.....CVPKPPKQMPKPPKPPK 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	449	22.3	1240	2 T05162	hypothetical prote
2	375.5	18.6	473	2 T19707	hypothetical prote
3	357.5	17.7	687	2 S51398	hypothetical prote
4	355	17.6	458	2 T38776	hypothetical prote
5	346	17.2	624	2 S67059	hypothetical prote
6	247.5	12.3	549	2 T33317	hypothetical prote
7	154.5	7.7	306	2 AH1769	conserved hypotet
8	139.5	6.9	306	2 AE1394	conserved hypotet
9	136.5	6.8	309	2 H69995	hypothetical prote
10	131	6.5	295	2 A83894	hypothetical prote
11	129.5	6.4	303	2 P69795	conserved hypotet
12	127	6.3	342	2 D86677	transcription regu
13	126	6.2	302	2 F86849	transcription regu
14	125.5	6.2	310	2 AG1665	hypothetical prote
15	122.5	6.1	311	2 F83871	multidrug resistan
16	122.5	6.1	364	2 F84898	hypothetical prote
17	120.5	6.0	310	2 A11293	hypothetical prote
18	118	5.9	309	2 AH1528	conserved hypotet
19	117	5.8	315	2 AB2166	hypothetical prote
20	113	5.6	309	2 AF1171	conserved hypotet
21	111	5.5	294	2 G95120	conserved hypotet
22	111	5.5	309	2 H70861	hypothetical prote
23	111	5.5	311	2 C97950	conserved hypotet
24	111	5.5	321	2 C70596	hypothetical prote
25	106	5.3	315	2 A89998	conserved hypotet
26	105.5	5.2	295	2 D83734	hypothetical prote
27	104	5.2	304	2 F72386	conserved hypotet
28	102	5.1	297	2 F69595	multidrug resistan
29	102	5.1	1273	2 E72611	probable ATP-depen

hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
gene retII protein
diacylglycerol kin
diacylglycerol kin
semaphorin C - mou
hypothetical prote
conserved hypotet
probable diacylgly
probable hydrolase
probable aminoadip
hypothetical prote
hypothetical prote
conserved hypotet

30 100.5 5.0 433 2 S75948
31 99 4.9 449 2 C83634
32 97.5 4.8 305 2 G89844
33 97 4.8 311 2 D75405
34 94 4.7 899 2 T38153
35 93.5 4.6 791 2 A46140
36 93.5 4.6 796 2 B46140
37 93 4.6 782 2 I48746
38 92.5 4.6 732 2 T16422
39 91.5 4.5 304 2 A86842
40 91.5 4.5 475 2 H84567
41 91 4.5 219 2 AE0724
42 91 4.5 981 2 T41029
43 91 4.5 1192 2 T17255
44 90.5 4.5 325 2 A97482
45 90.5 4.5 325 2 A12699

hypothetical protein F1885.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05162
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, August 1998
A:Reference number: Z15400
A:Accession: T05162
A:Molecule type: DNA
A:Residues: 1-1240 <BEV>
A:Cross-references: UNIPROT:O65419; EMBL:ALO22603
A:Experimental source: cultivar Columbia; BAC clone F1885
C:Genetics:
A:Map position: 4
A:Introns: 44/3; 117/3; 178/3; 206/1; 237/2; 375/1; 416/1; 449/3; 474/1; 503/1; 529/1; 5;
A:Note: F1885.160

Query Match 22.3%; Score 449; DB 2; Length 1240;
Best Local Similarity 31.9%; Pred. No. 2.2e-31;
Matches 122; Conservative 63; Mismatches 127; Indels 70; Gaps 13;

QY 11 LRPGRVLLNPRGKGKALQFRSHVQPLAAEISFTLMTERRNHARELVSEELG 70
DB 374 LGRPKRLVFPFGGKGKAREIFVKEVKPLFEDADVQLEIQETKYQLHAKFVKSMQVS 433
QY 71 RWDALVMSGDGLMHVEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVT 130
DB 434 KYDGIVCVSGDGLVEVNVNGLLERADRNALKLPFGVPAGTGNGMIKSLDVTGLRCCA 493
QY 131 NEDLLTNCILLCRLLSPNNLLSLHTAGBLRFSVLSLAWGFADVDLSEKYRLGEM 190
DB 494 N-----SATISIRGHKRSVDVATI-AQNTKFFSVMLAWGLIADIDIESEKFRWMSA 547
QY 191 RFTLGTFL-----RLAALRTYRCRLAYLPV-GRVGSKTPASPVVVQ- 230
DB 548 RIDFYVCLVDKFDNYCIAVVKLLALQRIICLRRYNGRIILFLPAPGEGVQOPASCSLYQE 607
QY 231 -----QGP-----VDAHLVPLPEPVSHWTVVVDLVLALLHS-HLGSE-MFA 274
DB 608 PHVSDKEVGVQGPETKFDLEWRMKGPFVTIW-----LHNVPWGSNTLT 653
QY 275 APMGRCAGVMHLFYRYAGVSRAMLLRLFLAMEKGMHEYECPIYVV-----FVVAFRL 329
DB 654 APAAKFSDGYLDLIVLK-NCPLKVLISLMRQTSSTGTHV--ESPVIYIKLTVEKVAFLV 710
QY 330 EP-----KDGKGMFAVDGELM 345
DB 711 EPGALVDEPKDKEGIIDSDGEVL 732

ALIGNMENTS

RESULT 1

T05162
hypothetical protein F1885.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05162
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, August 1998
A:Reference number: Z15400
A:Accession: T05162
A:Molecule type: DNA
A:Residues: 1-1240 <BEV>
A:Cross-references: UNIPROT:O65419; EMBL:ALO22603
A:Experimental source: cultivar Columbia; BAC clone F1885
C:Genetics:
A:Map position: 4
A:Introns: 44/3; 117/3; 178/3; 206/1; 237/2; 375/1; 416/1; 449/3; 474/1; 503/1; 529/1; 5;
A:Note: F1885.160

Query Match	7.7%; Score 154.5; DB 2; Length 306;	
Best Local Similarity	22.2%; Pred. No. 5.7e-06;	
Matches	77; Conservative 66; Mismatches 129; Indels 75; Gaps 16;	
Qy	16 RVLVLNPRGGKGKALQLFRSHVQPLLAEBISFTLMLTERRNHARELV--RSEELGRWD 73	
Db	4 KAMIIYNPAAGKGNKPKLL-PDAEKILTNADFEVTLVPSTPAKSTTTLIAQQAAG-YE 61	
Qy	74 ALVVMGSGGLMHEVNVGLME---RPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVT 130	
Db	62 VVIAAGDGTNEVNVGLMQVEKRP-----KLGIPLVGTNTDYARALNF----- 105	
Qy	131 NEDLITNCTLLRCRLLSPMNLLSLHTASGLRFLSVLSLAWGFADVDLESEKYRRLGEM 190	
Db	106 AKDPLEALQITIAKQETIR-----VDIGKANETEFF-INNAAGGRITEI----- 147	
Qy	191 RFTLGTFLRLAALRYRGRLAYLPVGRVSKTPASPVVVQGPVDHAHLVPLEEPVPVSHWT 250	
Db	148 -----TYAVKESMKSKWGLRAYLFSGLT-----VLPKLSPVNVVEIYNEE----- 187	
Qy	251 VVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLYFVRAGVSRAMLRLFLAMEKGR 310	
Db	188 IPKGBILLFFVNVKTSVGMETLCP-P-AQLNSGMPELLILKK-VSPKKLQOLFASIKKGT 245	
Qy	311 HMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELMVS-EAVQGQVHP 356	
Db	246 HL--NSPHVIHA-----RTNKTIKSDADLNVSVDGVYGGKAP 281	
RESULT 8		
AEI1394	conserved hypothetical protein lmo2557 [imported] - Listeria monocytogenes (strain EGD-e)	
C:Species:	Listeria monocytogenes	
C:Date:	27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C:Accession:	AEI1394	
A:	Glaser, P.; Brangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Kars, U. Science 294, 849-852, 2001	
A:Authors:	Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.	
A:Title:	Comparative genomics of Listeria species.	
A:Reference number:	AB1077; MUID:21537279; PMID:11679669	
A:Accession:	AEI1394	
A:Status:	preliminary	
A:Molecule type:	DNA	
A:Residues:	1-306 <GLA>	
A:Cross-references:	UNIPROT:O8Y497; GB:NC_003210; PIDN:CAD00635.1; PID:g16412045; GSPDB:	
A:Experimental source:	strain EGD-e	
C:Genetics:		
A:Gene:	lmo2557	
Query Match	6.9%; Score 139.5; DB 2; Length 306;	
Best Local Similarity	21.7%; Pred. No. 0.00012;	
Matches	76; Conservative 60; Mismatches 132; Indels 83; Gaps 16;	
Qy	16 RVLVLNPRGGKGKALQLFRSHVQPLLAEBISFTLMLTERRNHARELV--RSEELGRWD 73	
Db	4 KAMIIYNPAAGKGNKPKLL-PDAEKILTEANFEVTLVPSTPAKSTTTTIAQQAAG-FE 61	
Qy	74 ALVVMGSGGLMHEVNVGLMERPDWETAIOKP--LCSLPAGSGNALAASLNHYAGYEQVTN 131	
Db	62 VVIAAGDGTNEVNVGLMQ-----VDTPPKGLVLPVGTNTDYARALN-----FAKDPL 110	
Qy	132 EDLITNCTLLRCRLLSPMNLLSLHTASGLRL-FSVLSLAWGFADVDLESEKYRRLGEM 190	
Db	111 EAL-----RIIAKQETIRVDIGKANETEFFINNAAGKTKTEI----- 147	
Qy	191 RFTLGTFLRLAALRYRGRLAYLPVGRVSKTPASPVVVQGPVDHAHLVPLEEPVPVSHWT 250	
Db	148 -----TYAVKESMKSKWGLRAYLFSG-LTVLPKLSPVYVE-----I 182	

Qy	251 VVPDEDF-----VLVLLHSHLGSEMFAPMGRCAAGVMHLYFVRAGVSRAMLRLFLAM 306	
Db	183 AYNDIEIFGKILLFPVKNSSVGMETLCPPAELNSGNFELLILKK-VSPKKLQOLFASI 241	
Qy	307 EKRHMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELMVS-EAVQGQVHP 356	
Db	242 KKGTHL--SSPHVIHA-----RINKVTINSADADLNVSVDGVYGGKAP 281	
RESULT 9		
H6995	hypothetical protein ytlR - Bacillus subtilis	
C:Species:	Bacillus subtilis	
C:Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C:Accession:	H6995	
R:	Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrazi, E. Nature 390, 249-256, 1997	
A:Authors:	Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, tkeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A:Reference number: A69580; MUID:98044033; PMID:9384377	
A:Accession:	H6995	
A:Status:	preliminary; nucleic acid sequence not shown; translation not shown	
A:Molecule type:	DNA	
A:Residues:	1-309 <KUN>	
A:Cross-references:	UNIPROT:O34799; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14972.1	
A:Experimental source:	strain 168	
C:Genetics:		
A:Gene:	YtlR	
Query Match	6.8%; Score 136.5; DB 2; Length 309;	
Best Local Similarity	23.4%; Pred. No. 0.00023;	
Matches	79; Conservative 47; Mismatches 148; Indels 63; Gaps 17;	
Qy	20 LLNPRGGKALQLFRSHVQPLLAEBISFTLMTERNHARELVRS-----BELGRWDAL 75	
Db	7 IINPTAGHRNGRLRVKYS-IQELIKRKVEHRSFLTEPHGAFLVARQISTIQEY-KLKRL 64	
Qy	76 VVMGSDGLMHEVNVGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 135	
Db	65 IVTGGDGTMEHVNVGLKDVDDIE-----LSFVPAGAYNDFSRGFS-----IKKIDLI 111	
Qy	136 TNCTLLRCRLLSPMNLLSLHTASGLRLFSVLSLAWGFADVDLESEKYRRLGEMRFTLG 195	
Db	112 QE-----IKVKRPLT-RTEHLGS-VNFLQDKSQILYFMNHIGIFDAYVNVKKAAMEPLR 164	
Qy	196 ---TFLLAALRYRGRLAYLPVGRVSKTPASPVVVQGPVDHAHLVPLEEPVESH--WT 250	
Db	165 RVFLFLRL-----RFLVYPLSHLHASATFKFETLACTED-----ETREFHDVWF 209	
Qy	251 VVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLYFVRAGVSRAMLRLFL--AMEK 308	
Db	210 AVSN-----HPFYGGKKAAPLANPREKTFDIVIVE---NQPLFKYWLCLLMAF 257	
Qy	309 GRHMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELM 345	
Db	258 GKHTKMGVTFMFAKADITF--YTKD-KIPFHADGEIM 291	
RESULT 10		
A83894	hypothetical protein BH1953 [imported] - Bacillus halodurans (strain C-125)	
C:Species:	Bacillus halodurans	

Qy 292 AGVSRAMLRLFLAMEGRHMEYECPLYVTVVPVAFLEPKDQ-KGMFAVDGE 343
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
233 TD-NLFELIALLAIVANGKHL--DDVNLEYIKTSKIEIALEGQKILLNDGE 282

RESULT 13
F86849
transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Acession: F86849
R/Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: F86849
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-302 <STO>
A/Cross-references: UNIPROT:Q9CEN8; GB:AEO05176; PID:g12724823; PIDN:AAK05896.1; GSPDB:G-A/Experimental source: strain IL1403
C/Genetics:
A/Gene: ysfG

Query Match 6.2%; Score 126; DB 2; Length 302;
Best Local Similarity 21.2%; Pred. No. 0.0019;
Matches 75; Conservative 64; Mismatches 123; Indels 92; Gaps 17;

Qy 19 VLLNPRGGKGALQLFRSHVQPILAEAEISFTLMTERRNHARELYRS--EELGRWDALV 76
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
5 LLANPSGAGKGARTLETLI-PYLEKNYYEYRLFETKAAGEGVALVQIILDKNPDHLV 63

Qy 77 VMGDGLMHVEVNGLMERPDMETAIQKLCSLPAGSGNALAASL-----NHYAGYEQ 128
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
64 IIGDGITSLVINELPE-----EEAFSVIPSGSCNDFARSLKLDPIESFEAARRG 115

Qy 129 VTNEEDLTNTCLLCRRLLSPMNLLSHTASGLRFSVLWLANGFTADVDSSEKYRRLG 188
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
116 INHEIFIMN-----YQSKGLSGYALNNIGIGLDATI-VKSANEGLK 156

Qy 189 EM--RFTLGTFRLAALTVRGLAYLPVGRVGSKTTPASPVVVOQGVPDAHLVPLEPVP 246
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
157 QVLNKCLKGSF-----SYI-----LTALHVLTIKFPFA-LIEVEN--- 191

Qy 247 SHWTVPDEDFVLVALLHSHLGSEMFAAPMGRCACGVHMLFYVRAGVSRAMLLRFL-- 304
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
192 --QEISLEN AFLMTFKHPYFGGVKISP EATINAD IHL----VEYNKHLLRTFSLI 244

Qy 305 -AMEKGRHMEYECPLYVTVPVAFLEPKDQKGMFAVDGELMVSEAQQ--GVQH 355
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
245 PSVLRGHMLKH-----PFLHRVSPQ-----FSV--ELAESPQVIDGEIH 283

RESULT 14
AG1665
hypothetical protein homolog lin1865 [imported] - Listeria innocua (strain Clip11262)
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Acession: AG1665
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A./Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AG1665
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <GLA>
A/Cross-references: UNIPROT:Q92AQ5; GB:AL592022; PIDN:CAC97095.1; PID:g16414366; GSPDB:G-

A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1865

Query Match 6.2%; Score 125.5; DB 2; Length 310;
Best Local Similarity 21.3%; Pred. No. 0.0022;
Matches 74; Conservative 55; Mismatches 118; Indels 101; Gaps 15;

QY 19 VLLNPRGGKALKQRFSRSHVQPLLAEEF-----ISFTLMLTERRNHARELVSRSEELG 70
| : | | : : : : : : : : : : : : : : : : : :
DB 7 VIYNPTSGR---EIIKKNLADVLSSLEAQGVVTSAHATTAEPCDAKHAEEAVRD---- 58
| : | | : : : : : : : : : : : : : : : : : :
QY 71 RWDALVMSGDGLMHEVVNGLMERPDMWETAQKPLCSLPAGSGNALAAASLNHYAGYEQVT 130
| : | | : : | : | : | : | : | : | : | : | : | : | :
DB 59 RYDLVAAGDGTINEVGIAEQP-----YRPKGVIITGTTNDFA----- 100
| : | | : : : : : : : : : : : : : : : : : :
QY 131 NEDLLTNCTLLCRRLSPNNLLSIHTASGLRLFVSLSLAWGFADVDLESEKY----- 184
| : | | : : : : : : : : : : : : : : : : : :
DB 101 -----RALHVRPDV-----IKATKIIAAGQSIVAMDIGKANDTYFINIGG 139
| : | | : : : : : : : : : : : : : : : : : :
QY 185 -RRILGEMRFTLTGLRLRAALRTYGRRLAY-----LPVGRVGSKTTPASPVVVQQGPVDA 236
| : | | : : : : | : | : | : | : | : | : | :
DB 140 GGRLETETYDVP-----SRLKTMLGOLAYLYLKGIEMLP-----SLKATKVKEVDQG--- 186
| : | | : : : : : : : : : : : : : : : : : :
QY 237 HLVPLEEPVPSHWTVDPEDFVLVLALLHSLHGSEMFAAPMGRCAGVMHLFYVRAGVSR 296
| : | | : : : : : : : : : : : : : : : : : :
DB 187 -----VFGEVGMFFLLGLTNSIGGPEKI-APDAKLDDGKFSLIIVKK-VNL 230
| : | | : : : : : : : : : : : : : : : : : :
QY 297 AMLLRLFLAMEKGHMVECEPYLVYPVAFRLEPKDGKMPAVDDEL 344
| : | | : : : : : : | : | : | : | : | : | : | :
DB 231 AEFIRLVTLALRGDHIKE--PNVIYVKSEKVSVHSED-KMLINLDGEL 275
| : | | : : : : : : : : : : : : : : : : : :

RESULT 15
F83871
multidrug resistance protein bmrU [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F83871
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirano,
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <STO>
A;Cross-references: UNIPROT.Q9KC00; GB:BA001513; GB:BA000004; NID:g10174345; PIDN:BAB054
A;Experimental source: strain C-125
C;Genetics:
A;Gene: bmrU

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Query Match      6.1%; Score 122.5; DB 2; Length 311;  
Best Local Similarity 30.5%; Pred. No. 0.0041;  
Matches 32; Conservative 17; Mismatches 47; Indels 9; Gaps 3;  
  
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Search completed: June 15, 2005, 12:03:16
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2005, 12:02:38 ; Search time 157 Seconds
(without alignments)
937.582 Million cell updates/sec

Title: US-10-642-289-2

Perfect score: 2017

Sequence: 1 MDPAGRGVLPKPCRVLVL.....CVRPPSWKQPMPPPERPL 384

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2017	100.0	384	16	US-10-642-289-2
2	2013	99.8	384	9	US-09-970-516-2
3	2013	99.8	384	14	US-10-354-358-26
4	2013	99.8	384	15	US-10-619-344-2
5	2005	99.4	384	9	US-09-796-487-3
6	2005	99.4	384	16	US-10-723-860-722
7	2004	99.4	384	17	US-10-479-933-1
8	1996	99.0	398	16	US-10-715-117-2
9	1959	97.1	384	9	US-09-784-810A-2
10	1920	95.2	368	14	US-10-053-510-21
11	1920	95.2	368	15	US-10-348-052-21

12	1920	95.2	368	16	US-10-622-011-21	Sequence 21, Appl
13	1749	86.7	333	15	US-10-264-237-2585	Sequence 2585, Ap
14	1636.5	81.1	382	9	US-09-784-810A-4	Sequence 4, Appli
15	1629.5	80.8	382	9	US-09-970-516-6	Sequence 6, Appli
16	1629.5	80.8	382	15	US-10-619-344-6	Sequence 6, Appli
17	1627.5	80.7	388	9	US-09-817-676A-15	Sequence 15, Appl
18	1627.5	80.7	388	9	US-09-796-487-2	Sequence 2, Appli
19	1627.5	80.7	388	16	US-10-830-677-15	Sequence 15, Appl
20	1624.5	80.5	381	9	US-09-796-487-1	Sequence 1, Appli
21	1624.5	80.5	381	9	US-09-796-487-4	Sequence 4, Appli
22	1606.5	79.6	373	9	US-09-796-487-5	Sequence 5, Appli
23	1538	76.3	293	10	US-09-933-767-328	Sequence 328, App
24	1538	76.3	293	14	US-10-004-860-328	Sequence 328, App
25	1538	76.3	293	14	US-10-023-282-328	Sequence 9, Appli
26	935.5	46.4	204	9	US-09-796-487-9	Sequence 12, Appl
27	894	44.3	617	9	US-09-817-676A-12	Sequence 12, Appl
28	894	44.3	617	16	US-10-830-677-12	Sequence 14, Appl
29	883.5	43.8	618	9	US-09-817-676A-14	Sequence 4, Appli
30	883.5	43.8	618	9	US-09-970-516-4	Sequence 78, Appl
31	883.5	43.8	618	14	US-10-354-358-78	Sequence 4, Appli
32	883.5	43.8	618	15	US-10-619-344-4	Sequence 14, Appl
33	883.5	43.8	618	15	US-10-830-677-14	Sequence 14, Appl
34	883.5	43.8	618	16	US-10-737-450-140	Sequence 140, App
35	830.5	41.2	638	10	US-09-969-896-3	Sequence 3, Appli
36	830.5	41.2	638	16	US-10-631-958-3	Sequence 3, Appli
37	560	27.8	490	14	US-10-053-510-19	Sequence 19, Appl
38	560	27.8	490	15	US-10-348-052-19	Sequence 19, Appl
39	560	27.8	490	16	US-10-622-011-19	Sequence 19, Appl
40	560	27.8	490	15	US-10-348-052-28	Sequence 28, Appl
41	560	27.8	641	16	US-10-622-011-28	Sequence 28, Appl
42	519.5	25.8	524	14	US-10-053-510-20	Sequence 20, Appl
43	519.5	25.8	524	15	US-10-348-052-20	Sequence 20, Appl
44	519.5	25.8	524	16	US-10-622-011-20	Sequence 20, Appl
45	519.5	25.8	907	15	US-10-348-052-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-10-642-289-2
; Sequence 2, Application US/10642289
; Publication No. US20040132053A1
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON-1
; CURRENT APPLICATION NUMBER: US/10/642,289
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/959,897
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-642-289-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 LEEPVPSHWTVVPDDEFVLVLLALHSHLGSEMFAPMGRCAGVMHLPVVRAGVSRAML 300
QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVQGVHPNYFW 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVQGVHPNYFW 360
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Db 361 MVSGCVERPPSPKQPMPPPEPL 384
RESULT 2
US-09-970-516-2
; Sequence 2, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-516-2

Query Match 99.8%; Score 2013; DB 9; Length 384;
Best Local Similarity 99.7%; Pred. No. 2.9e-189;
Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 361 MVSGCVERPPSPKQPMPPPEPL 384
Db 361 MVSGCVERPPSPKQPMPPPEPL 384
RESULT 3
US-10-354-358-26
; Sequence 26, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14224, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; FILE REFERENCE: MPI02-020P1ENOMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-26

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Best Local Similarity 99.7%; Pred. No. 2.9e-189;
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; Sequence 2, Application US/10619344
; Publication No. US20040086487A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/10/619,344
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/970,516
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-344-2

Query Match 99.8%; Score 2013; DB 15; Length 384;
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Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 361 MVSGCVBPPPSWKPPQMPPEEPL 384
RESULT 5
US-09-796-487-3
; Sequence 3, Application US/09796487
; Patent No. US20020042358A1
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase. Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(384)
; OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspo
; OTHER INFORMATION: nding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of Ge
; OTHER INFORMATION: nbank sequence Accession Number AAF73423.
; PUBLICATION INFORMATION:
; AUTHORS: Nava et al.
; TITLE: Functional characterization of human sphingosine kinase-1
; JOURNAL: FEBS Lett.
; VOLUME: 473
; ISSUE: 1
; PAGES: 81-84
; DATE: 2000
; DATABASE ACCESSION NUMBER: AAF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AFF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
US-09-796-487-3

Query Match 99.4%; Score 2005; DB 9; Length 384;
Best Local Similarity 99.0%; Pred. No. 1.8e-188;
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DB 181 SEKYYRLGEMRFTLGTFLRLAALTYRGLAYLPVGRVSGKTPASPVVVQQGPVDALHP 240
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QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDCKGMAFVADGELMVSEAVQGVHPNFW 360
DB 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDCKGMAFVADGELMVSEAVQGVHPNFW 360

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QY 361 MVSGCVERPPSWKPKQMPPEPL 384
Db 361 MVSGCVERPPSWKPKQMPPEPL 384

RESULT 6
US-10-723-860-722
; Sequence 722, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 722
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-722

Query Match 99.4%; Score 2005; DB 16; Length 384;
Best Local Similarity 99.0%; Pred. No. 1.8e-188;
Matches 380; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDPAGGPRGVLPKRCVLVLLNPRGGKQKALQLFRRSHVQPLLAERAEISFTMLTERRNHA 60

QY 61 RELVRSSELGRWDALVVMGSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSELGRWDALVVMGSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120

QY 121 NHYAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRFLSVLSLANGFTADVLE 180
Db 121 NHYAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRFLSVLSLANGFTADVLE 180

QY 181 SEKVRRLGEMRFTLGTFLRLAALTYRGLAYLPVGRVGSKTPASPVVVVQGPVDHLVP 240
Db 181 SEKVRRLGEMRFTLGTFLRLAALTYRGLAYLPVGRVGSKTPASPVVVVQGPVDHLVP 240

QY 241 LEEPVPSSHWTVPDDEDFVLVLLALSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPSSHWTVPDDEDFVLVLLALSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAML 300

QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVOGQHPNYFW 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVOGQHPNYFW 360

RESULT 7
US-10-479-933-1
; Sequence 1, Application US/10479933
; Publication No. US20050100547A1
; GENERAL INFORMATION:
; APPLICANT: Xia, Pu
; APPLICANT: Wang, Lijun
; APPLICANT: Vadas, Mathew
; APPLICANT: Gamble, Jennifer
; APPLICANT: Moretti, Paul
; APPLICANT: Pitson, Stuart
```

```
; TITLE OF INVENTION: SPHINGOSINE KINASE INTERACTS WITH TRAF2 AND
; TITLE OF INVENTION: MODULATES TUMOR NECROSIS FACTOR-INDUCED CELLULAR
; FILE REFERENCE: 650063.401USPC
; CURRENT APPLICATION NUMBER: US/10/479,933
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/AU02/00710
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 354
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-479-933-1

Query Match 99.4%; Score 2004; DB 17; Length 384;
Best Local Similarity 99.2%; Pred. No. 2.2e-188;
Matches 381; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPKRCVLVLLNPRGGKQKALQLFRRSHVQPLLAERAEISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPKRCVLVLLNPRGGKQKALQLFRRSHVQPLLAERAEISFTMLTERRNHA 60

QY 61 RELVRSSELGRWDALVVMGSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSELGRWDALVVMGSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120

QY 121 NHYAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRFLSVLSLANGFTADVLE 180
Db 121 NHYAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRFLSVLSLANGFTADVLE 180

QY 181 SEKVRRLGEMRFTLGTFLRLAALTYRGLAYLPVGRVGSKTPASPVVVVQGPVDHLVP 240
Db 181 SEKVRRLGEMRFTLGTFLRLAALTYRGLAYLPVGRVGSKTPASPVVVVQGPVDHLVP 240

QY 241 LEEPVPSSHWTVPDDEDFVLVLLALSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPSSHWTVPDDEDFVLVLLALSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAML 300

QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVOGQHPNYFW 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMVSEAVOGQHPNYFW 360

QY 361 MVSGCVERPPSWKPKQMPPEPL 384
Db 361 MVSGCVERPPSWKPKQMPPEPL 384

RESULT 8
US-10-715-117-2
; Sequence 2, Application US/10715117
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANXIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
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; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-2

Query Match
Best Local Similarity 99.0%; Score 1996; DB 16; Length 398;
Matches 383; Conservative 1; Mismatches 0; Indels 14; Gaps 1;

Qy 1 MDP-----AGGPRGVLPKRCVVLVLLNPRGGKGKALQLFRSHVQPLLAAB 46
Db 1 MDPVVCGCGRLFGFVSAGGPRGVLPKRCVVLVLLNPRGGKGKALQLFRSHVQPLLAAB 60

Qy 47 ISFTMLTERRNHARELVRSEBELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLC 106
Db 61 ISFTMLTERRNHARELVRSEBELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLC 120

Qy 107 SLPAGSGNALAASLNHYAGYEQTNEDLLTNCTLLLCRLLSPMNLLSLHTASGLRLFSV 166
Db 121 SLPAGSGNALAASLNHYAGYEQTNEDLLTNCTLLLCRLLSPMNLLSLHTASGLRLFSV 180

Qy 167 LSLANGFTADVLESEKYRRLGEMFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASP 226
Db 181 LSLANGFTADVLESEKYRRLGEMFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASP 240

Qy 227 VVQQGPVDALHVPLEEPVPSHTVVPDEDVFLVLLALHSHLGSEMPAAMPGRCAAGVMH 286
Db 241 VVQQGPVDALHVPLEEPVPSHTVVPDEDVFLVLLALHSHLGSEMPAAMPGRCAAGVMH 300

Qy 287 LFVVRAGVSRAMLLRLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMV 346
Db 301 LFVVRAGVSRAMLLRLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMV 360

Qy 347 SEAVQGVHPNTFWMVSGCVPEPPSPKQMPPEPL 384
Db 361 SEAVQGVHPNTFWMVSGCVPEPPSPKQMPPEPL 398

RESULT 9
US-09-784-810A-2
; Sequence 2, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-810A-2

Query Match
Best Local Similarity 97.4%; Score 1959; DB 9; Length 384;
Matches 374; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MDPAGGPRGVLPKRCVVLVLLNPRGGKGKALQLFRSHVQPLLAABEISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPKRCVVLVLLNPRGGKGKALQLFRSHVQPLLAABEISFTMLTERRNHA 60

Qy 61 RELVRSEELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVRSEELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASL 120
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Qy 121 NHYAGYEQVTNEDLLTNCTLLLCRLLSPMNLLSLHTASGLRLFSVLSLANGFTADVLE 180
Db 121 NHYAGYEQVTNEDLLTNCTLLLCRVLSPMNLLSLHTASGLRSLVLSLANGFTADVLE 180

Qy 181 SEKTRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASPVVVQQGPVDALHVP 240
Db 181 SDKYRRLGEMRFTLGTFLRLAALRTYRGLATLPVGRVGFKTASPVVVQQGPVDALHVP 240

Qy 241 LEEPVPSSHWTVPDDEDVFLVLLALHSHLGSEMPAAMPGRCAAGVMHLPFYVRAGVSRAMLL 300
Db 241 LEEQVPSSHQVVPDDEDVFLVLLALHSHLASEMPAAMPGRCAAGVMHLPFYVRAGVSRAMLL 300

Qy 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNTFWMV 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNTFWMV 360

Qy 361 MVSGCVPEPPSPKQMPPEPL 384
Db 361 MVSGCVPEPPSPKQMPPEPL 384

RESULT 10
US-10-053-510-21
; Sequence 21, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Eyrst, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-510-21

Query Match
Best Local Similarity 95.2%; Score 1920; DB 14; Length 368;
Matches 367; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 VLVLLNPRGGKGKALQLFRSHVQPLLAABEISFTMLTERRNHARELVRSEELGRWDALV 76
Db 1 VLVLLNPRGGKGKALQLFRSHVQPLLAABEISFTMLTERRNHARELVRSEELGRWDALV 60

Qy 77 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
Db 61 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120

Qy 137 NCTLLLCRLLSPMNLLSLHTASGLRLFSVLSLANGFTADVLESEKYRRLGEMRFTLGT 196
Db 121 NCTLLLCRLLSPMNLLSLHTASGLRLFSVLSLANGFTADVLESEKYRRLGEMRFTLGT 180

Qy 197 FLRLAALRTYRGLAYLPVGRVSKTPASPVVVQQGPVDALHVPLEEPVPSHTVVPDED 256
Db 181 FLRLAALRTYRGLAYLPVGRVSKTPASPVVVQQGPVDALHVPLEEPVPSHTVVPDED 240

Qy 257 FVLVLLALHSHLGSEMPAAMPGRCAAGVMHLPFYVRAGVSRAMLLRLFLAMEKGRHMEYEC 316
Db 241 FVLVLLALHSHLGSEMPAAMPGRCAAGVMHLPFYVRAGVSRAMLLRLFLAMEKGRHMEYEC 300

Qy 317 PVLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNTFWMVSGCVPEPPSPKQ 376
Db 301 PVLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNTFWMVSGCVPEPPSPKQ 360

Qy 377 MPPPEPL 384
Db 361 MPPPEPL 368
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RESULT 11
US-10-348-052-21
; Sequence 21, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348,052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-052-21

Query Match      95.2%; Score 1920; DB 15; Length 368;
Best Local Similarity 99.7%; Pred. No. 3.9e-180;
Matches 367; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLVLLNPRGGKQKALQLFRSHVQPLLAEEAETISFTMLTERRNHARELVRSEELGRWDALV 76
Db 1 VLVLLNPRGGKQKALQLFRSHVQPLLAEEAETISFTMLTERRNHARELVRSEELGRWDALV 60

QY 77 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
Db 61 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120

QY 137 NCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKYRRLGEMRFTLTGT 196
Db 121 NCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKYRRLGEMRFTLTGT 180

QY 197 FLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGPVDAHLVPLEEPVPSHWTVPDDED 256
Db 181 FLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGPVDAHLVPLEEPVPSHWTVPDDED 240

QY 257 FVLVLALLHSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 316
Db 241 FVLVLALLHSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 300

QY 317 PVLVYVPVVAFRLEPKDKGKMFVADGELMVSEAVQGVHPNYFMVSGCVPEPPPSWKPPQ 376
Db 301 PVLVYVPVVAFRLEPKDKGKMFVADGELMVSEAVQGVHPNYFMVSGCVPEPPPSWKPPQ 360

QY 377 MPPPEEPL 384
Db 361 MPPPEEPL 368

RESULT 12
US-10-264-237-2585
; Sequence 2585, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Bitse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131p1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2585
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2585

Query Match      86.7%; Score 1749; DB 15; Length 333;
Best Local Similarity 99.7%; Pred. No. 2.4e-163;
Matches 332; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 52 MLTERRNHARELVRSEELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAG 111
Db 1 MLTERRNHARELVRSEELGRWDALVMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAG 60

QY 112 SGNALAASLNHYAGYEQVTNEDLLTNCCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAW 171
Db 61 SGNALAASLNHYAGYEQVTNEDLLTNCCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAW 120

QY 172 GFTADVLESEKYRRLGEMRFTLTGTFLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQ 231
Db 121 GFTADVLESEKYRRLGEMRFTLTGTFLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQ 180

QY 232 GPVDAHLVPLEEPVPSHWTVPDDED FVLVLALLHSHLGSMEFAAPMGRCAAGVMHLFVR 291
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RESULT 11
US-10-348-052-21
; Sequence 21, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348,052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-052-21

Query Match      95.2%; Score 1920; DB 15; Length 368;
Best Local Similarity 99.7%; Pred. No. 3.9e-180;
Matches 367; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLVLLNPRGGKQKALQLFRSHVQPLLAEEAETISFTMLTERRNHARELVRSEELGRWDALV 76
Db 1 VLVLLNPRGGKQKALQLFRSHVQPLLAEEAETISFTMLTERRNHARELVRSEELGRWDALV 60

QY 77 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
Db 61 VMSGDGLMHEVVNGLMERPDMETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120

QY 137 NCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKYRRLGEMRFTLTGT 196
Db 121 NCTLLCRRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKYRRLGEMRFTLTGT 180

QY 197 FLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGPVDAHLVPLEEPVPSHWTVPDDED 256
Db 181 FLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGPVDAHLVPLEEPVPSHWTVPDDED 240

QY 257 FVLVLALLHSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 316
Db 241 FVLVLALLHSHLGSMEFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 300

QY 317 PVLVYVPVVAFRLEPKDKGKMFVADGELMVSEAVQGVHPNYFMVSGCVPEPPPSWKPPQ 376
Db 301 PVLVYVPVVAFRLEPKDKGKMFVADGELMVSEAVQGVHPNYFMVSGCVPEPPPSWKPPQ 360

QY 377 MPPPEEPL 384
Db 361 MPPPEEPL 368

RESULT 12
US-10-622-011-21
; Sequence 21, Application US/10622011
; Publication No. US20040126834A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405C1
; CURRENT APPLICATION NUMBER: US/10/622,011
; CURRENT FILING DATE: 2003-07-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-011-21
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Db 181 GPDALHLEPEVSHWTVVPEDEFLVLLHSHLGSEFAAPMGRCAGVWHLFVVR 240
QY 292 AGVSRAMLRLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGKMPAIDGELMVSEAVQ 351
Db 241 AGVSRAMLRLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGKMPAIDGELMVSEAVQ 300
QY 352 GOVHNYFMWVSGVEPPSWKPOQMPPEEP 384
Db 301 GOVHNYFMWVSGVEPPSWKPOQMPPEEP 333

RESULT 14
US-09-784-810A-4
; Sequence 4, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-784-810A-4

Query Match 81.1%; Score 1636.5; DB 9; Length 382;
Best Local Similarity 80.7%; Pred. No. 3.5e-152;
Matches 309; Conservative 34; Mismatches 39; Indels 1; Gaps 1;
QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQLFQSRVQPFLEAEISFTMLTERRNHA 60
Db 1 MEPVECPGRLPRPCRVLLNPRGGKQKALQLFQSRVQPFLEAEISFTMLTERRNHA 60
QY 61 RELVRSSELGRWDALVVMGSGDGLMHEVYVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVCAEELGHWDALAVMSGDGLMHEVYVNGLMERPDWETAIOKPLCSLPAGSGNALAASV 120
QY 121 NHYAGYEQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
QY 181 SEKRYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVP 240
Db 181 SEKRYRLGEIRFTVGTFFRLASRLIYQQLAYLPVGTAVSKRPAS-TLVQKGPVDTHLVP 239
QY 241 LEEPVPSSHWTVPDEDFVLVLLHSHLGSEFAAPMGRCAGVWHLFVYRAGVSRAALL 300
Db 240 LEEPVPSSHWTVPDEDFVLVLLHSHLGSEFAAPMGRCAGVWHLFVYRAGVSRAALL 299
QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGKMPAIDGELMVSEAVQGVHPNYFW 360
Db 300 RLFLAMQKGMELDCPYLVHVPVAFRLPEPRSGRVFSDGGLMVCEAVQGVHPNYLW 359
QY 361 MVSGCVPEPPSWKPOQMPPEEP 383
Db 360 MVCSRDAPSGRDSRRGPPPEEP 382

RESULT 15
US-09-970-516-6
; Sequence 6, Application US/09970516
; Patent No. US2002009029A1
; GENERAL INFORMATION:

; APPLICANT: No. US2002009029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-970-516-6

Query Match 80.8%; Score 1629.5; DB 9; Length 382;
Best Local Similarity 80.4%; Pred. No. 1.7e-151;
Matches 308; Conservative 34; Mismatches 40; Indels 1; Gaps 1;
QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQLFQSRVQPFLEAEISFTMLTERRNHA 60
Db 1 MEPVECPGRLPRPCRVLLNPRGGKQKALQLFQSRVQPFLEAEISFTMLTERRNHA 60
QY 61 RELVRSSELGRWDALVVMGSGDGLMHEVYVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVCAEELGHWDALAVMSGDGLMHEVYVNGLMERPDWETAIOKPLCSLPAGSGNALAASV 120
QY 121 NHYAGYEQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
QY 181 SEKRYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVP 240
Db 181 SEKRYRLGEIRFTVGTFFRLASRLIYQQLAYLPVGTAVSKRPAS-TLVQKGPVDTHLVP 239
QY 241 LEEPVPSSHWTVPDEDFVLVLLHSHLGSEFAAPMGRCAGVWHLFVYRAGVSRAALL 300
Db 240 LEEPVPSSHWTVPDEDFVLVLLHSHLGSEFAAPMGRCAGVWHLFVYRAGVSRAALL 299
QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPEPKDGKMPAIDGELMVSEAVQGVHPNYFW 360
Db 300 RLFLAMQKGMELDCPYLVHVPVAFRLPEPRSGRVFSDGGLMVCEAVQGVHPNYLW 359
QY 361 MVSGCVPEPPSWKPOQMPPEEP 383
Db 360 MVCSRDAPSGRDSRRGPPPEEP 382

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Job time : 159 secs

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OM protein - protein search, using sw model

Run on: June 15, 2005, 11:52:11 ; Search time 163 Seconds
(without alignment)
911.141 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 2017
Sequence: 1 MDPAGPRGVLPKPCRVLVL.....CVEPPPSWKPPQMPPEPL 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04: *
1: Geneseqp19808: *
2: Geneseqp19908: *
3: Geneseqp20008: *
4: Geneseqp20018: *
5: Geneseqp20028: *
6: Geneseqp20038a: *
7: Geneseqp20038b: *
8: Geneseqp20048: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2017	100.0	384	4	AAB48007 Human sph
2	2017	100.0	384	7	ADF28783 Human sph
3	2013	99.8	384	3	AAB18659 A human r
4	2013	99.8	384	4	AAB94589 Human pro
5	2013	99.8	384	4	AAB93955 Human pro
6	2013	99.8	384	4	AAB00924 Human sph
7	2013	99.8	384	5	ABG31586 Human sph
8	2013	99.8	384	7	ADE38365 Human pro
9	2008	99.6	384	4	AAM40180 Human pol
10	2005	99.4	384	5	ABB08089 Human sph
11	2005	99.4	384	8	ADQ17905 Human sof
12	2004	99.4	384	6	ABP71054 Human sph
13	1997	99.0	384	3	AAV96057 Human sph
14	1996	99.0	398	8	ADJ75441 Marker ge
15	1996	99.0	398	8	ADJ75387 Marker ge
16	1996	99.0	398	8	ADO22417 Human sph
17	1959	97.1	384	4	AAE07882 Human sph
18	1920	95.2	368	6	ABR82391 Human sph
19	1749	86.7	333	5	ABB90209 Human pol
20	1636.5	81.1	382	4	AAE07883 Human sph
21	1629.5	80.8	382	5	ABG31588 Mouse sph
22	1627.5	80.7	388	3	AAV56054 Mouse sph
23	1627.5	80.7	388	5	ABB08088 Murine sph
24	1627.5	80.7	388	8	ADJ76219 Marker ge
25	1624.5	80.5	381	3	AAV56053 Mouse sph

26	1624.5	80.5	381	5	ABB08087 Murine sp
27	1624.5	80.5	381	5	ABB08090 Murine sp
28	1608	79.7	305	4	AAM41966 Human pol
29	1606.5	79.6	373	5	ABB08091 Murine sp
30	1538	76.3	293	2	AAW88613 Secreted
31	1538	76.3	293	4	ABB50380 Human sec
32	1538	76.3	293	6	ABO44637 Novel hum
33	1538	76.3	293	7	ABO26117 Human pro
34	1077.5	53.4	260	4	ABU52807 Human sph
35	935.5	46.4	204	5	ABB08095 Human sph
36	894	44.3	617	4	AU09073 Mouse sph
37	886.5	44.0	618	4	AAU09075 Human sph
38	883.5	43.8	618	4	AAU09074 Human sph
39	883.5	43.8	618	5	ABG31587 Human sph
40	883.5	43.8	618	5	ABB07855 Protein s
41	883.5	43.8	618	7	ADE38417 Human can
42	883.5	43.8	618	8	ADQ15182 Human can
43	883.5	43.8	654	4	ABU52806 Human sig
44	883.5	43.8	654	8	ADJ66569 Sphingosi
45	870.5	43.2	806	4	ABG21144 Novel hum

ALIGNMENTS

RESULT 1
AAB48007
ID AAB48007 standard; protein; 384 AA.

XX
AC AAB48007;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human sphingosine kinase protein sequence.
XX
KW Sphingosine kinase; antiarthritic; antiasthmatic; antiarteriosclerotic;
KW antiinflammatory; neuroprotective; antibacterial; immunosuppressive;
KW human.
XX
OS Homo sapiens.
XX
PN WO200070028-A1.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-AU000457.
XX
PR 13-MAY-1999; 99AU-00000339.
PR 08-JUL-1999; 99AU-00001504.
XX
XX (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Pitson SM, Wattenberg BW, Xia P, D'andrea RJ, Gamble JR;
PI Vadas MA;
XX
XX WPI: 2001-016227/02.
DR N-PSDB; AAC84161.
DR
XX Novel sphingosine kinase protein and nucleic acid molecules for
XX diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma,
PT atherosclerosis, inflammation, meningitis, multiple sclerosis and septic
PT shock.
XX
PS Claim 9; Fig 7a; 100pp; English.
XX
XX This represents a human sphingosine kinase (SK) protein. The human SK
XX protein, encoding nucleic acids and modulators are useful for modulating
XX expression, functional activity or cellular functional activity of
XX sphingosine kinase in a subject and also for treating a mammal by
XX modulating the activity of SK. Diseases treated by regulating SK cellular
XX activity include rheumatoid arthritis, asthma, atherosclerosis,
XX inflammation, meningitis, multiple sclerosis and septic shock

```
SQ      Sequence 384 AA;
Query Match      100.0%; Score 2017; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 7.5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPAGGPRGVLP RPRCRVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
      |||
DB      1 MDPAGGPRGVLP RPRCRVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
      |||

QY      61 RELVSEELGRWDALVVMGSGDGLMHEVVGMLERPDWETA IQKPLCSLPAGSGNALAASL 120
      |||
DB      61 RELVSEELGRWDALVVMGSGDGLMHEVVGMLERPDWETA IQKPLCSLPAGSGNALAASL 120
      |||

QY      121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNL LSLHTASGLR LFSVLSLAWGFIADV DLE 180
      |||
DB      121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNL LSLHTASGLR LFSVLSLAWGFIADV DLE 180
      |||

QY      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||
DB      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||

QY      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||
DB      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||

QY      241 LEEPVP SHWTVVPDED FVLV LALLSHL GSEMFAAPMGRCAAGVMHLF YVRAGVSRAMLL 300
      |||
DB      241 LEEPVP SHWTVVPDED FVLV LALLSHL GSEMFAAPMGRCAAGVMHLF YVRAGVSRAMLL 300
      |||

QY      301 RLFLAMEKGRHMEYEC PLYLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
      |||
DB      301 RLFLAMEKGRHMEYEC PLYLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
      |||

QY      361 MVSGC VEPSPSKWKPQMPPEEPL 384
      |||
DB      361 MVSGC VEPSPSKWKPQMPPEEPL 384
      |||
```

```
RESULT 2
ADF28783
ID      ADF28783 standard; protein; 384 AA.
XX      AC      ADF28783;
XX      DT      12-FEB-2004 (first entry)
XX      DE      Human sphingosine kinase (hSK)1 protein sequence.
XX      KW      SK; sphingosine kinase; phosphorylation; protein kinase; ERK1; ERK2;
XX      KW      CDK2; cytosolic; antiinflammatory; immunosuppressive; antiarthritic;
XX      KW      antirheumatic; antiarteriosclerotic; antiasthmatic; human; hSK1; enzyme.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
FT      Modified-site 148      /note= "phosphorylated"
FT      Modified-site 181      /note= "phosphorylated"
FT      Modified-site 184      /note= "phosphorylated"
FT      Modified-site 225      /note= "phosphorylated"
FT      Modified-site 250      /note= "phosphorylated"
FT      Modified-site 250      /note= "phosphorylated"
XX      FN      WO2003082322-A1.
XX      PD      09-OCT-2003.
XX      PF      28-MAR-2003; 2003WO-AU0000388.
XX      PR      28-MAR-2002; 2002AU-00001448.
XX      PR      05-APR-2002; 2002AU-00001538.
XX      PR      08-APR-2002; 2002AU-00001621.
XX      PR      19-SEP-2002; 2002AU-00951668.
```

```
PR      21-JAN-2003; 2003AU-00900230.
XX      PA      (MEDV-) MEDVET SCI PTY LTD.
XX      PI      Pitson SM, Xia P, Moretti PA, Verwey JR, Vadas MA, Wattenberg BW;
XX      WPI; 2003-803967/75.
XX      Modulating sphingosine kinase functional activity for treating arthritis,
XX      atherosclerosis and asthma by contacting the sphingosine kinase with an
XX      agent for a time and under conditions to modulate phosphorylation of the
XX      kinase.
XX      Example 2; SEQ ID NO 12; 95pp; English.
XX      The invention relates to modulating sphingosine kinase (SK) functional
XX      activity. The method involves contacting the SK with an agent for a time
XX      and under conditions to modulate phosphorylation of the SK where inducing
XX      or agonizing the phosphorylation upregulates the SK activity and
XX      inhibiting or antagonizing the phosphorylation down regulates the SK
XX      activity. The modulation of the phosphorylation is modulation of proline-
XX      directed protein kinase catalyzed phosphorylation. The proline-directed
XX      kinase is ERK1, ERK2 or CDK2. The modulation is preferably down-
XX      regulation. The methods and agents are useful for treating and/or
XX      prophylaxis of a condition characterized by aberrant, unwanted or
XX      inappropriate cellular activity or sphingosine kinase functional
XX      activity, e.g. a neoplastic condition or an inflammatory condition such
XX      as rheumatoid arthritis, atherosclerosis, asthma, autoimmune disease or
XX      inflammatory bowel disease. The present sequence represents a human SK
XX      (hSK)1 protein.
```

SQ Sequence 384 AA;

```
Query Match      100.0%; Score 2017; DB 7; Length 384;
Best Local Similarity 100.0%; Pred. No. 7.5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPAGGPRGVLP RPRCRVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
      |||
DB      1 MDPAGGPRGVLP RPRCRVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHA 60
      |||

QY      61 RELVSEELGRWDALVVMGSGDGLMHEVVGMLERPDWETA IQKPLCSLPAGSGNALAASL 120
      |||
DB      61 RELVSEELGRWDALVVMGSGDGLMHEVVGMLERPDWETA IQKPLCSLPAGSGNALAASL 120
      |||

QY      121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNL LSLHTASGLR LFSVLSLAWGFIADV DLE 180
      |||
DB      121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNL LSLHTASGLR LFSVLSLAWGFIADV DLE 180
      |||

QY      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||
DB      181 SEK YRLGEMRFTLGTFRLAALRTYGR LAYLPVGRVSKTPASP VVVVQQGPVD AHLVP 240
      |||

QY      241 LEEPVP SHWTVVPDED FVLV LALLSHL GSEMFAAPMGRCAAGVMHLF YVRAGVSRAMLL 300
      |||
DB      241 LEEPVP SHWTVVPDED FVLV LALLSHL GSEMFAAPMGRCAAGVMHLF YVRAGVSRAMLL 300
      |||

QY      301 RLFLAMEKGRHMEYEC PLYLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
      |||
DB      301 RLFLAMEKGRHMEYEC PLYLVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
      |||

QY      361 MVSGC VEPSPSKWKPQMPPEEPL 384
      |||
DB      361 MVSGC VEPSPSKWKPQMPPEEPL 384
      |||
```

```
RESULT 3
AAB18659
ID      AAB18659 standard; protein; 384 AA.
XX      AC      AAB18659;
XX      DT      22-JAN-2001 (first entry)
```


XX	DE	A human regulator of intracellular phosphorylation.
XX	KW	Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
XX	KW	neurological disorder; Parkinson's disease; demyelinating disease;
KW	KW	meningitis; developmental disorder; neuromuscular disorder; cancer;
KW	KW	myasthenia gravis; cell proliferative disorder; actinic keratosis;
KW	KW	arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis;
KW	KW	autoimmune disorder; inflammatory disorder; Addison's disease;
KW	KW	acquired immunodeficiency disease; allergy; diabetes mellitus;
KW	KW	rheumatoid arthritis; microbial infection; trauma.
XX	OS	Homo sapiens.
XX	XX	
XX	Key	Location/Qualifiers
XX	FT	Active-site
FT	FT	/note= "16..153
FT	FT	/note= "diacylglycerol kinase catalytic site"
FT	FT	Modified-site
FT	FT	/note= "54
FT	FT	/note= "potential phosphorylation site"
FT	FT	Modified-site
FT	FT	/note= "130
FT	FT	/note= "potential phosphorylation site"
FT	FT	Modified-site
FT	FT	/note= "137
FT	FT	/note= "potential glycosylation site"
FT	FT	Modified-site
FT	FT	/note= "181
FT	FT	/note= "potential phosphorylation site"
FT	FT	Modified-site
FT	FT	/note= "205
FT	FT	/note= "potential phosphorylation site"
FT	FT	Modified-site
FT	FT	/note= "371
FT	FT	/note= "potential phosphorylation site"
XX	XX	
PN	XX	WO20005332-A2.
XX	XX	
PD	PD	21-SEP-2000.
XX	XX	
PF	PF	17-MAR-2000; 2000WO-US007277.
XX	XX	
PR	XX	18-MAR-1999; 99US-0125593P.
XX	XX	20-MAY-1999; 99US-0135049P.
PR	PR	09-JUL-1999; 99US-0143188P.
XX	XX	
XX	XX	(INCY-) INCYTE PHARM INC.
PA	XX	
XX	XX	Bandman O, Tang YT, Yue H, Hillman JL, Baughn MR, Azimzai Y;
PI	PI	Lu DAM, Au-Young J;
PI	PI	WPI: 2000-602121/57.
DR	XX	N-PSDB; AAA75676.
DR	XX	
XX	XX	Novel human intracellular phosphorylation regulator polypeptides and
FT	FT	polynucleotides for diagnosis, prevention and treatment of neurological,
PT	PT	cell proliferative and autoimmune/inflammatory disorders.
XX	XX	
PS	PS	Claim 1; Page 77-78; 96pp; English.
XX	XX	
CC	CC	The present sequence represents a human regulator of intracellular
CC	CC	phosphorylation (HRIP). HRIP is useful for screening agonists and
CC	CC	antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are
CC	CC	useful for treating a disease or condition associated with decreased or
CC	CC	increased expression of functional HRIP. Diseases treated or diagnosed
CC	CC	include neurological disorders such as stroke, Parkinson's disease,
CC	CC	demyelinating diseases, bacterial and viral meningitis and other
CC	CC	developmental disorders of the central nervous system, neuromuscular
CC	CC	disorders, myasthenia gravis, cell proliferative disorders such as
CC	CC	actinic keratosis, arteriosclerosis, atherosclerosis and cancer including
CC	CC	leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder,
CC	CC	bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory
CC	CC	disorder such as Addison's disease, acquired immunodeficiency diseases,
CC	CC	allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial
CC	CC	infection and trauma
XX	XX	
SQ	SQ	Sequence 384 AA;

CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 384 AA;

Query Match 99.8%; Score 2013; DB 4; Length 384;
 Best Local Similarity 99.7%; Pred. No. 2e-209;
 Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 QY 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 Db 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 QY 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 Db 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 QY 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 Db 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 QY 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300
 Db 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300
 QY 301 RLFLAMEKGRHWEYECPLVYVPVVAFLPEKDGKMFVAVDGLMVSEAVOGVHPNYFW 360
 Db 301 RLFLAMEKGRHWEYECPLVYVPVVAFLPEKDGKMFVAVDGLMVSEAVOGVHPNYFW 360
 QY 361 MVSGCVERPPSKQPMPPPEPL 384
 Db 361 MVSGCVERPPSKQPMPPPEPL 384

RESULT 5
 AAB93955
 ID AAB93955 standard; protein; 384 AA.
 XX
 AC AAB93955;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:13997.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX

PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 13997; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 384 AA;

Query Match 99.8%; Score 2013; DB 4; Length 384;
 Best Local Similarity 99.7%; Pred. No. 2e-209;
 Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 QY 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 Db 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 QY 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 Db 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 QY 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 Db 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 QY 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300
 Db 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

Query Match 99.8%; Score 2013; DB 4; Length 384;
 Best Local Similarity 99.7%; Pred. No. 2e-209;
 Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAETISFTLMLTERRNHA 60
 QY 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 Db 61 RELVRSEELGRWDALVVMGSDGLMHVNVGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
 QY 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 Db 121 NHYAGYEQVTNEDLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
 QY 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 Db 181 SEKVRRLGEMRFTLTGFLRLAALRYRGLAYLPVGRVGSKTPTASPVVVOGQPVDAHLVP 240
 QY 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300
 Db 241 LEEPVPSSHWTVPDDEDFVLVLLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

QY 301 RLFLAMEKGRHMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNFW 360
 Db 301 RLFLAMEKGRHMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNFW 360

QY 361 MVSGCVPPEPPSWKPPQMPPEPL 384
 Db 361 MVSGCVPPEPPSWKPPQMPPEPL 384

RESULT 6
 AAE00924
 ID AAE00924 standard; protein; 384 AA.

XX AAE00924;
 XX
 DT 04-JUL-2001 (first entry)

XX Human sphingosine kinase type 1 (hskl).

XX Human; sphingosine kinase type 1; skl; chromosome 17q25.2;
 KW sphingosine-1-phosphate; SIP; drug screening; therapy; haemostasis;
 KW thrombosis; allergic reaction; proliferative disease; cancer;
 KW haematopoietic disorder; leukaemia; cardiovascular disease; stroke;
 KW atherosclerosis; coronary artery disease; dyslipidaemia; diabetes;
 KW autoimmune disease; inflammatory disease; multiple sclerosis;
 KW T helper-1 related disease; chronic obstructive pulmonary disease;
 KW asthma; myocardial infarction; neurodegenerative disorder; wound healing;
 KW embryogenesis; anticoagulant; cerebroprotective; neuroprotective;
 KW antipsoriatic; antiarthritic; cytostatic; cardiac; vulnary.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 16..95
 FT /label= Conserved_region

XX WO200131029-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-EP009498.

XX 28-OCT-1999; 99US-0162307P.

XX 07-FEB-2000; 2000US-0180525P.

XX (WARN) WARNER LAMBERT CO.

XX Allen J, Gosink M, Melendez AJ, Takacs L;

XX WPI; 2001-300510/31.
 DR N-PSDB; AAD04477.

XX New human sphingosine kinase type I gene for screening drug candidates

XX particularly inhibitors used for preventing or treating e.g.

XX atherosclerosis, thrombosis, asthma and diabetes.

XX Claim 3; Fig 1; 91pp; English.

XX The present sequence is human sphingosine kinase type 1 (hskl). The hsk1
 CC gene is located on chromosome 17q25.2. The skl converts the substrate
 CC sphingosine to sphingosine-1-phosphate (SIP). The skl gene and encoded
 CC polypeptide are applicable in screening drug candidates particularly
 CC inhibitors for preventing or treating disorders such as haemostasis,
 CC thrombosis, allergic reactions, proliferative diseases including cancer,
 CC haematopoietic disorders such as leukaemia, cardiovascular diseases such
 CC as stroke, atherosclerosis and coronary artery disease, dyslipidaemia,
 CC diabetes including type I and type II diabetes, autoimmune and
 CC inflammatory diseases such as multiple sclerosis, T helper-1 related
 CC diseases, chronic obstructive pulmonary disease, asthma, myocardial
 CC infarction, neurodegenerative disorders, natural wound healing processes
 CC and embryogenesis

XX Sequence 384 AA;

Query Match 99.8%; Score 2013; DB 4; Length 384;
 Best Local Similarity 99.7%; Pred. No. 2e-209;
 Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPFCRVLVLLNPRGGKGAQLFRSHVQPLLAETISFTLMLTERRNHA 60
 Db 1 MDPAGGPRGVLPFCRVLVLLNPRGGKGAQLFRSHVQPLLAETISFTLMLTERRNHA 60

QY 61 RELVRSEELGRWDALVWMSGDGLMHEVVGMLWRPDMETAIQKPLCSLPAGSGNALAASL 120
 Db 61 RELVRSEELGRWDALVWMSGDGLMHEVVGMLWRPDMETAIQKPLCSLPAGSGNALAASL 120

QY 121 NHYAGYEQVTNEDLLTNCTLLCRLLSPMNLSSHTASGLRFLSVLSLAWGFADVDLE 180
 Db 121 NHYAGYEQVTNEDLLTNCTLLCRLLSPMNLSSHTASGLRFLSVLSLAWGFADVDLE 180

QY 181 SEKYRRLGEMRFTLTGFLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGVDAHLVP 240
 Db 181 SEKYRRLGEMRFTLTGFLRLAALRTYRGLAYLPVGRVSGKTPASPVVVOQGVDAHLVP 240

QY 241 LEEPVPSTWTVVDDDFVLVLLALHSHLGSEMAAPMGRCAGVMHLFVVRAGVSRMLL 300
 Db 241 LEEPVPSTWTVVDDDFVLVLLALHSHLGSEMAAPMGRCAGVMHLFVVRAGVSRMLL 300

QY 301 RLFLAMEKGRHMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNFW 360
 Db 301 RLFLAMEKGRHMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNFW 360

QY 361 MVSGCVPPEPPSWKPPQMPPEPL 384
 Db 361 MVSGCVPPEPPSWKPPQMPPEPL 384

RESULT 7
 ABG31586
 ID ABG31586 standard; protein; 384 AA.

XX ABG31586;

XX 05-NOV-2002 (first entry)

XX Human sphingosine kinase 1 (SPHK1).

XX Human; sphingosine kinase 1; SPHK1; blood vessel formation; primate;
 KW congestive heart failure; myocardial ischaemia; wound healing;
 KW ischaemia-reperfusion injury; peripheral arterial disease; angiogenesis;
 KW coronary artery disease; peripheral vascular disease; fracture repair;
 KW reconstructive surgery; transplantation; islet transplant; tendon repair;
 KW sports injury; ulcer; thromboangitis obliterans; Buerger's disease;
 KW periodontal tissue regeneration; radiotherapy-induced oesophagitis.

XX Homo sapiens.

XX WO200228406-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-EP011513.

XX 05-OCT-2000; 2000US-0238230P.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Liao G, Stefansson S, Su J;

XX WPI; 2002-608171/65.

XX N-PSDB; ABK90198.

XX Inducing blood vessel formation, or preventing/treating congestive heart
 PT failure, ischemia-reperfusion injury, myocardial ischemia and peripheral
 PT arterial diseases in animal, by administering sphingosine kinase.

XX PS Disclosure; Page 35-36; 45pp; English.

XX CC The present invention relates to a new method of inducing blood vessel

CC formation in an animal. The method of the invention involves

CC administering sphingosine kinase to the animal. The method is useful for

CC inducing blood vessel formation in an animal, or preventing or treating

CC congestive heart failure, myocardial ischaemia, ischaemia-reperfusion

CC injury and peripheral arterial diseases in an animal, e.g. mammal (such

CC as primate including human). The invention is also useful for treating

CC diseases or disorders selected from coronary artery disease, peripheral

CC vascular disease, wound healing and fracture repair, reconstructive

CC surgery, transplantation such as islet transplants, tendon repair/sports

CC injury, healing of ulcers, thromboangitis obliterans (Buerger's disease),

CC periodontal tissue regeneration and radiotherapy-induced oesophagitis.

CC The present amino acid sequence represents the human sphingosine kinase 1

CC (SPHK1) protein as described in the invention

XX Sequence 384 AA;

Query Match 99.8%; Score 2013; DB 5; Length 384;

Best Local Similarity 99.7%; Pred. No. 2e-209;

Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAGGPRGVLPKRCRVLLNPRGGKQKALQLFESHVQPLLAEEAIEFTMLTERRNHA 60

Db 1 MDPAGGPRGVLPKRCRVLLNPRGGKQKALQLFESHVQPLLAEEAIEFTMLTERRNHA 60

Qy 61 RELVSEELGRWDALVVMGSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

Db 61 RELVSEELGRWDALVVMGSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

Qy 121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVDLE 180

Db 121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVDLE 180

Qy 181 SEKYLGEGRMFTLTGFLRLAALTYRGLAYLPVGRVSKTPASPVVVOGQPDVAHLVP 240

Db 181 SEKYLGEGRMFTLTGFLRLAALTYRGLAYLPVGRVSKTPASPVVVOGQPDVAHLVP 240

Qy 241 LEEPVSHWTVPDDEFLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

Db 241 LEEPVSHWTVPDDEFLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

Qy 301 RLFLAMEGRHMEYECPLVYVVPVAFRLEPKDKGMPAVDGLMVSVAOQVHPNYFW 360

Db 301 RLFLAMEGRHMEYECPLVYVVPVAFRLEPKDKGMPAVDGLMVSVAOQVHPNYFW 360

Qy 361 MVSGCVPEPPSWKPOQMPPEPL 384

Db 361 MVSGCVPEPPSWKPOQMPPEPL 384

RESULT 8

ADE38365

ID ADE38365 standard; protein; 384 AA.

AC ADE38365;

XX 29-JAN-2004 (first entry)

XX Human protein 49863 amino acid sequence.

XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;

XX aberrant protein activity; cytostatic; antithyroid; antidiabetic;

XX ophthalmological; cancer; breast cancer; colon cancer; lung cancer;

XX prostatic cancer; Grave's disease; diabetic retinopathy; protein 49863.

OS Homo sapiens.

XX WO2003065006-A2.

XX 07-AUG-2003.

PD

XX 30-JAN-2003; 2003WO-US002588.

XX 31-JAN-2002; 2002US-0353600P.

PR 15-MAR-2002; 2002US-0364517P.

PR 09-APR-2002; 2002US-0371075P.

PR 10-APR-2002; 2002US-0371507P.

PR 16-APR-2002; 2002US-0372984P.

PR 19-APR-2002; 2002US-0374194P.

PR 24-MAY-2002; 2002US-0382995P.

PR 31-MAY-2002; 2002US-0385023P.

PR 14-JUN-2002; 2002US-0388853P.

PR 17-JUN-2002; 2002US-0389395P.

PR 25-JUN-2002; 2002US-0391324P.

PR 15-JUL-2002; 2002US-0395944P.

PR 22-JUL-2002; 2002US-039726P.

PR 13-AUG-2002; 2002US-0403046P.

PR 22-AUG-2002; 2002US-0405155P.

PR 27-AUG-2002; 2002US-0406361P.

PR 25-OCT-2002; 2002US-0421195P.

PR 12-NOV-2002; 2002US-0425456P.

PR 19-NOV-2002; 2002US-0427626P.

PR 10-DEC-2002; 2002US-0432122P.

XX (MILL-) MILLENNIUM PHARM INC.

PA Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;

XX Williamson MW, Rudolph-Owen LA;

PI WPI: 2003-646176/61.

XX N-PSDB; ADE38364.

DR

DR

XX

PT Treating subject having tumorigenic disorder or angiogenic disorder

PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic

PT acid, by administering a modulator.

XX Disclosure; SEQ ID NO 26; 454pp; English.

XX This invention relates to a novel method of treating a human subject

CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant

CC gene expression or activity of an isolated protein, by administering a

CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic

CC or ophthalmological activity. The method is useful for treating a subject

CC having a tumorigenic or angiogenic disorder, in particular for treating

CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic

CC cancer) and, for example, Grave's disease and diabetic retinopathy. The

CC present sequence is the amino acid sequence of the novel isolated human

CC protein 49863 of the invention.

XX Sequence 384 AA;

Query Match 99.8%; Score 2013; DB 7; Length 384;

Best Local Similarity 99.7%; Pred. No. 2e-209;

Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAGGPRGVLPKRCRVLLNPRGGKQKALQLFESHVQPLLAEEAIEFTMLTERRNHA 60

Db 1 MDPAGGPRGVLPKRCRVLLNPRGGKQKALQLFESHVQPLLAEEAIEFTMLTERRNHA 60

Qy 61 RELVSEELGRWDALVVMGSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

Db 61 RELVSEELGRWDALVVMGSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

Qy 121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVDLE 180

Db 121 NHYAGYEQVTNEDLLTNTCLLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFIADVDLE 180

Qy 181 SEKYLGEGRMFTLTGFLRLAALTYRGLAYLPVGRVSKTPASPVVVOGQPDVAHLVP 240

Db 181 SEKYLGEGRMFTLTGFLRLAALTYRGLAYLPVGRVSKTPASPVVVOGQPDVAHLVP 240

Qy 241 LEEPVSHWTVPDDEFLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

Db 241 LEEPVSHWTVPDDEFLVLALHSLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML 300

Db 241 LEEPVPSHWTVVDEDFVLVLLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECFYLVPVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Db 301 RLFLAMEKGRHMEYECFYLVPVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Qy 361 MVSGCVPPEPPSWKPPQMPPEEPL 384
Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 9
AAW40180
ID AAW40180 standard; protein; 384 AA.
XX AAW40180;
XX
XX 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 3325.
XX
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
OS
XX
XX W0200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00489725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI59336.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 5; SEQ ID NO 3325; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAW38642-AAW42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
SQ Sequence 384 AA;
Query Match 99.6%; Score 2008; DB 4; Length 384;
Best Local Similarity 99.5%; Pred. No. 7.2e-209;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDPAGGPRGVLPRPCRVLLNPRGGKALQLFRSHVQPLLAELISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPRPCRVLLNPRGGKALQLFRSHVQPLLAELISFTMLTERRNHA 60
Qy 61 RELVSEELGRWDALVVMGDLMEHVYVNGLMERPDWETAIOKPLCPLPAGSGNALAPSL 120
Db 61 RELVSEELGRWDALVVMGDLMEHVYVNGLMERPDWETAIOKPLCPLPAGSGNALAPSL 120
Qy 121 NHYAGYEQTNEEDLLTNCTLLCRLLSPMNLISLHTASGLRFLSVLSLANGFIADVDLE 180
Db 121 NHYAGYEQTNEEDLLTNCTLLCRLLSPMNLISLHTASGLRFLSVLSLANGFIADVDLE 180
Qy 181 SEKYEELGEMRFTLCTFLRLAALTYRGLAYLPVGRVSKTPASPVVVOQGVDAHLVP 240
Db 181 SEKYEELGEMRFTLCTFLRLAALTYRGLAYLPVGRVSKTPASPVVVOQGVDAHLVP 240
Qy 241 LEEPVPSHWTVVDEDFVLVLLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPSHWTVVDEDFVLVLLSHLGSSEMFAPMGRCAGVMHLFYVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECFYLVPVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Db 301 RLFLAMEKGRHMEYECFYLVPVVAFLRLEPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Qy 361 MVSGCVPPEPPSWKPPQMPPEEPL 384
Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 10
ABB08089
ID ABB08089 standard; protein; 384 AA.
XX ABB08089;
XX
XX 10-SEP-2002 (first entry)
DT
XX Human sphingosine kinase 1 (hSPHK1) protein sequence.
DE
XX Sphingosine kinase; SPHK; SPHK1; cytosolic; vasotropic; antidiabetic;
KW neuroprotective; human; enzyme.
XX
XX Homo sapiens.
OS
XX US2002042358-A1.
PN
XX 11-APR-2002.
PD
XX 02-MAR-2001; 2001US-00796487.
PF
XX 02-MAR-2000; 2000US-0186352P.
PR
XX (SPIE/) SPIEGEL S.
PA
XX Spiegel S;
PI
XX WPI; 2002-478846/51.
DR
XX New isolated sphingosine kinase, useful in identifying modulators for
PT treating e.g. Cancer, also related nucleic acid, vectors and transformed
PT cells.
XX
XX Disclosure; Fig 3; 24pp; English.
PS
XX

CC The invention relates to an isolated sphingosine kinase (SPHK) DNA. Cells
CC transformed with SPHK DNA are used to screen for agents that reduce,
CC eliminate or promote SPHK activity. Agents that inhibit activity are
CC useful for decreasing cell proliferation, e.g. for treating cancer, and
CC for treating diseases associated with abnormal migration and motility of
CC cells, e.g. restenosis or diabetic neuropathy. Agents that increase
CC activity are used to reduce cell death. Antibodies raised against SPHK,
CC and primers or oligonucleotides derived from the DNA are useful for
CC diagnosis. The antibodies are also useful as therapeutic inhibitors. The
CC present sequence represents a human sphingosine kinase 1 (hsPHK1)
XX
SQ Sequence 384 AA;

Query Match 99.4%; Score 2005; DB 5; Length 384;
Best Local Similarity 99.0%; Pred. No. 1.5e-208;
Matches 380; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDPAGGPRGVLPKRCVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHA 60
Db 1 MDPAGGPRGVLPKRCVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHA 60
Qy 61 RELVRSSELGRWDALVVMGSGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSELGRWDALVVMGSGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Qy 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Qy 181 SEKRYRLGEMRFTLTGTLRLAALRYRGLAYLPVGRVGSKTTPASPVVQQGPVDAHLVP 240
Db 181 SEKRYRLGEMRFTLTGTLRLAALRYRGLAYLPVGRVGSKTTPASPVVQQGPVDAHLVP 240
Qy 241 LEEPVPSHWTVVDPEDFVLVLLSHLGSEMFAAPMGRCAAGVMHLYFVRAGVSRAML 300
Db 241 LEEPVPSHWTVVDPEDFVLVLLSHLGSEMFAAPMGRCAAGVMHLYFVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Qy 361 MVSGCVPPEPPSWKPPQMPPEEPL 384
Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 11
ADQ17905
ID ADQ17905 standard; protein; 384 AA.
XX
AC ADQ17905;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 722.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
OS WPI; 2004-441208/41.

XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 722; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 384 AA;

Query Match 99.4%; Score 2005; DB 8; Length 384;
Best Local Similarity 99.0%; Pred. No. 1.5e-208;
Matches 380; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDPAGGPRGVLPKRCVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHA 60
Db 1 MDPAGGPRGVLPKRCVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHA 60
Qy 61 RELVRSSELGRWDALVVMGSGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSELGRWDALVVMGSGDLMEHVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Qy 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Qy 181 SEKRYRLGEMRFTLTGTLRLAALRYRGLAYLPVGRVGSKTTPASPVVQQGPVDAHLVP 240
Db 181 SEKRYRLGEMRFTLTGTLRLAALRYRGLAYLPVGRVGSKTTPASPVVQQGPVDAHLVP 240
Qy 241 LEEPVPSHWTVVDPEDFVLVLLSHLGSEMFAAPMGRCAAGVMHLYFVRAGVSRAML 300
Db 241 LEEPVPSHWTVVDPEDFVLVLLSHLGSEMFAAPMGRCAAGVMHLYFVRAGVSRAML 300
Qy 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Db 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
Qy 361 MVSGCVPPEPPSWKPPQMPPEEPL 384
Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 12
ABP71054
ID ABP71054 standard; protein; 384 AA.
XX
AC ABP71054;
XX
DT 14-APR-2003 (first entry)
XX
DE Human sphingosine kinase.
XX
KW TNF; tumour necrosis factor; sphingosine kinase; TRAP; TRAP2; cytostatic;
KW TNF receptor-associated factor; antinflammatory; antirheumatic; human;
KW antiarthritic.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Misc-difference 354 /note= "Xaa is unknown"
FT Region 379. .382
FT FT /note= "specifically claimed peptide"
XX
XX WO200298458-A1.
XX
XX 12-DEC-2002.
XX
XX 03-JUN-2002; 2002WO-AU000710.
XX
XX 07-JUN-2001; 2001AU-00005521.
XX
XX 13-AUG-2001; 2001AU-00006978.
XX
XX 27-DEC-2001; 2001AU-00009759.
XX
XX (MEDV-) MEDVET SCI PTY LTD.
XX
XX Xia P, Wang L, Vadaas M, Gamble J, Moretti P, Pitson S;
XX
XX WPI; 2003-201282/19.
XX
XX Modulating cytokine- or tumor necrosis factor-induced cellular activity,
XX useful for treating or preventing a neoplastic condition, comprises
XX modulating an intracellular sphingosine kinase-dependent signaling
XX mechanism.
XX
XX Claim 8; Fig 9; 96pp; English.
XX
XX The invention relates to modulating cytokine-induced or tumor necrosis
XX factor (TNF)-induced cellular activity. The method involves contacting
XX the cell with an agent under conditions sufficient to modulate the
XX interaction of sphingosine kinase with a TNF receptor-associated factor
XX (TRAF), preferably TRAF2, where inducing the association up-regulates
XX cellular activity, and inhibiting the association down-regulates cellular
XX activity. The agent is useful for manufacturing a medicament for treating
XX a mammal with a condition of aberrant, unwanted or inappropriate cytokine
XX -induced or TNF-induced cellular activity. The methods are useful for
XX modulating cytokine-induced or TNF-induced cellular activity, or for
XX treating or preventing a condition of aberrant, unwanted or inappropriate
XX cytokine-induced or TNF-induced cellular activity in a mammal, such as
XX neoplastic condition or inflammation (e.g. rheumatoid arthritis). The
XX present sequence represents a human sphingosine kinase
XX
XX Sequence 384 AA;
XX
XX Query Match 99.4%; Score 2004; DB 6; Length 384;
XX Best Local Similarity 99.2%; Pred. No. 1.9e-208;
XX Matches 381; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTMLTERRNHA 60
XX
XX 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTMLTERRNHA 60
XX
XX 61 RELVSEELGRWDALVVMGDLVHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
XX
XX 61 RELVSEELGRWDALVVMGDLVHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
XX
XX 121 NHVAGYEQVTNEDLLTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
XX
XX 121 NHVAGYEQVTNEDLLTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
XX
XX 181 SEKYYRLGEMRFTLTGTFRLAALRTYGRLAYLPVGRVSGKTPASPVVQQGPVDAHLVP 240
XX
XX 181 SEKYYRLGEMRFTLTGTFRLAALRTYGRLAYLPVGRVSGKTPASPVVQQGPVDAHLVP 240
XX
XX 241 LEEPVPSHWTVDPDEDVFLVLLALHSLGSEMAAPMGRCAGVMHLLFYVRAGVSAMLL 300
XX
XX 241 LEEPVPSHWTVDPDEDVFLVLLALHSLGSEMAAPMGRCAGVMHLLFYVRAGVSAMML 300
XX
XX 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMWSEAVQOQHFNYPW 360
XX
XX 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDQKGMFAVDGELMWSEAVQOQHFNYPW 360

QY 361 MVSGCVBPPPSWKPQOMPPPEPL 384
Db 361 MVSGCVBPPPSWKPQOMPPPEPL 384
RESULT 13
AAY96057
ID AAY96057 standard; protein; 384 AA.
XX
XX AAY96057;
XX
XX 05-DEC-2000 (first entry)
XX
XX Human sphingosine kinase A.
XX
XX Sphingosine kinase A; SKA; human; drug screening; infection;
XX antiinflammatory; antiallergic; anticancer; inflammation; allergy;
XX cancer; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX WO200052173-A2.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-CA000223.
XX
XX 02-MAR-1999; 99US-0122516P.
XX (ALIX) NPS ALLELIX CORP.
XX
XX Munroe D, Gupta A, Falzone GR;
XX
XX WPI; 2000-572185/53.
XX N-PSDB; AAA50508.
XX
XX New human sphingosine kinase A, B and C polynucleotides and polypeptides
XX useful in e.g. chromosome and gene mapping, and detecting inflammation or
XX disease associated with abnormal levels of sphingosine kinase expression.
XX
XX Disclosure; Fig 3; 81pp; English.
XX
XX The present sequence is that of human sphingosine kinase A (SKA), an
XX enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate.
XX The sequence was deduced from that of a polynucleotide (see AAA50508)
XX isolated from an HeLa cDNA library. The invention provides
XX polynucleotides (see AAA50508-10) and polypeptides (see AAY96057-59) for
XX the human sphingosine kinase (SK) homologues SKA, SKB and SKC. The
XX polypeptides can be obtained using recombinant DNA methods, and host
XX cells containing expression vectors including SK polynucleotides are used
XX in a claimed method of screening for compounds that inhibit or activate
XX human SK activity. Human SK specific antibodies, inhibitors, ligands or
XX their analogues can be used as bioactive agents to treat inflammation or
XX disease including viral, bacterial or fungal infections, allergic
XX responses, mechanical injury associated with trauma, hereditary diseases,
XX lymphoma or carcinoma, and other conditions with activate the genes of
XX kidney, lung, heart, lymphoid or tissues of the nervous system
XX
XX Sequence 384 AA;
XX
XX Query Match 99.0%; Score 1997; DB 3; Length 384;
XX Best Local Similarity 99.0%; Pred. No. 1.1e-207;
XX Matches 380; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTMLTERRNHA 60
XX
XX 1 MDPAGGPRGVLPRPCRVLLNPRGGKGKALQFRSHVQPLLAEEISFTMLTERRNHA 60
XX
XX 61 RELVSEELGRWDALVVMGDLVHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
XX
XX 61 RELVSEELGRWDALVVMGDLVHVEVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120

QY 121 NHYAGVEQVNTDILLTNCRLLSPMNLLSLHTASGLRLFSVLAWGFIADVDLE 180
 DB 121 NHYAGVEQVNTDILLTNCRLLSPMNLLSLHTASGLRLFSVLAWGFIADVDLE 180
 QY 181 SEKYRLGEMRFTLCTFLRLAALRTYRGLAYLPVGRVSKTPASPVPVVOQGPVDHLVP 240
 DB 181 SEKYRLGEMRFTLCTFLRLAALRTYRGLAYLPVGRVSKTPASPVPVVOQGPVDHLVP 240
 QY 241 LEEPVPSHWTVVPDDEDFVLVLLSHLSEMFAPMGRCAGVMHLPYVRAGVSRAMLL 300
 DB 241 LEEPVPSHWTVVPDDEDFVLVLLSHLSEMFAPMGRCAGVMHLPYVRAGVSRAMLL 300
 QY 301 RLFLAMEKGRHMEYPCPYLVVVPVAFRLPKDGMFAVDGELMVSBAVQGVHPNFVW 360
 DB 301 RLFLAMEKGRHMEYPCPYLVVVPVAFRLPKDGMFAVDGELMVSBAVQGVHPNFVW 360
 QY 361 MYSGCVERPPSWKPPQMPPEEPL 384
 DB 361 MYSGCVERPPSWKPPQMPPEEPL 384
 RESULT 14
 ADJ75441
 ID ADJ75441 standard; protein; 398 AA.
 XX
 AC ADJ75441;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:693.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EPI394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX
 DR WPI; 2004-193155/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Example 11; SEQ ID NO 693; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising to a portion of
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (f) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 398 AA;
 Query Match 99.0%; Score 1996; DB 8; Length 398;
 Best Local Similarity 96.2%; Pred. No. 1.5e-207;
 Matches 383; Conservative 1; Mismatches 0; Indels 14; Gaps 1;
 QY 1 MDP-----AGGPRGVLPVPCRVLLNPRGGKALQLFRRSHVQPLLAEE 46
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 DB 61 ISFTMLTERRNHARELVRSSEELGRWDALVVMGSDGLMHEVNGLMERPDPWETAIOKPLC 120
 QY 107 SLPAGSGNALAASLNHYAGVEQVNTDILLTNCRLLSPMNLLSLHTASGLRFSV 166
 DB 121 SLPAGSGNALAASLNHYAGVEQVNTDILLTNCRLLSPMNLLSLHTASGLRFSV 180
 QY 167 LSLAWGFIADVDLESEKRYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASP 226
 DB 181 LSLAWGFIADVDLESEKRYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTPASP 240
 QY 227 VVVOQGPVDHLVPLEEPVFSHWTVVPDDEDFVLVLLSHLSEMFAPMGRCAGVMH 286
 DB 241 VVVOQGPVDHLVPLEEPVFSHWTVVPDDEDFVLVLLSHLSEMFAPMGRCAGVMH 300
 QY 287 LFYVRAGVSRAMLLRLFLAMEKGRHMEYPCPYLVVVPVAFRLPKDGMFAVDGELMV 346
 DB 301 LFYVRAGVSRAMLLRLFLAMEKGRHMEYPCPYLVVVPVAFRLPKDGMFAVDGELMV 360
 QY 347 SEAVQGVHPNYFMVSGCVERPPSWKPPQMPPEEPL 384
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 ADJ75387
 ID ADJ75387 standard; protein; 398 AA.
 XX
 AC ADJ75387;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:639.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EPI394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX

PR 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX (GENO-) GENOX RES INC.
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
DR
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
PS Example 11; SEQ ID NO 639; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (1) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 398 AA;
Query Match 99.0%; Score 1996; DB 8; Length 398;
Best Local Similarity 96.2%; Pred. No. 1.5e-207;
Matches 383; Conservative 1; Mismatches 0; Indels 14; Gaps 1;
QY 1 MDP-----AGGPRGVLPRPCRVLLNPRGGKQKALQLFRRSHVQPLLAEE 46
DB 1 MDPVVGCGRLFGFVSAGSGPRGVLPRPCRVLLNPRGGKQKALQLFRRSHVQPLLAEE 60
QY 47 ISFTLMLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVNGLMERPDWETAIOKPLC 106
DB 61 ISFTLMLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVNGLMERPDWETAIOKPLC 120
QY 107 SLPAGSNGALAAHNYHAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRLFSV 166
DB 121 SLPAGSNGALAAHNYHAGYEQVTNEDLLTNCILLCRLLSPMNLISLHTASGLRLFSV 180
QY 167 LSLAWGFADVDLESEKRYRLGEMRFTLGTFLRLAALRYRGLAYLIPVGRVSKTPASP 226
DB 181 LSLAWGFADVDLESEKRYRLGEMRFTLGTFLRLAALRYRGLAYLIPVGRVSKTPASP 240
QY 227 VVVOQGPVDAHLVPLEEPVPSHMTVPDEDFVLVLLHSHLGSEMPAAMPGRCAAGVMH 286
DB 241 VVVOQGPVDAHLVPLEEPVPSHMTVPDEDFVLVLLHSHLGSEMPAAMPGRCAAGVMH 300
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Job time : 166 secs

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OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 03:38:14 ; Search time 237 Seconds
(without alignments)
8319.466 Million cell updates/sec

Title: US-10-642-289-1

Perfect score: 1205

Sequence: 1 gaattcgacagagcg.....gatctagatgcacctgcag 1205

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
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- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1205	100.0	1205	4	US-09-959-897-1
2	1162.6	96.5	1783	4	US-09-949-016-1155
3	1149.4	95.4	1533	4	US-09-205-258-90
4	1147	95.2	1155	4	US-09-970-516-1
5	1081.4	89.7	1764	4	US-09-949-016-3940
6	774.4	64.3	7195	4	US-09-949-016-12897
7	774.4	64.3	7198	4	US-09-949-016-15682
8	760	63.1	1149	4	US-09-970-516-5
9	491.4	40.8	601	4	US-09-949-016-40620
10	491.4	40.8	601	4	US-09-949-016-139382
11	258	21.4	1857	4	US-09-970-516-3
12	258	21.4	2380	4	US-09-817-676A-13
13	245.2	20.3	2698	4	US-09-817-676A-11
14	111.2	9.2	10550	4	US-09-949-016-17081
15	78.6	6.5	1012	4	US-09-270-767-12677
16	59.8	5.0	831	4	US-09-270-767-14024
17	52	4.3	191	4	US-09-270-767-28485
18	51.2	4.2	4432	4	US-09-774-528-148
19	50.2	4.2	2187	4	US-09-902-540-3500
20	50.2	4.2	18471	4	US-09-902-540-1167
21	49.8	4.1	1170	4	US-09-902-540-5823
22	49.8	4.1	72704	4	US-09-902-540-1273
23	48.8	4.0	2793	1	US-08-209-747-1
24	48.8	4.0	2793	1	US-08-458-298-1
25	47.8	4.0	900	5	PCT-US95-04801-3
26	47	3.9	3168	4	US-09-902-540-8270
27	47	3.9	8090	4	US-09-902-540-855

28	46.6	3.9	1413	4	US-09-902-540-5411	Sequence 5411, Ap
29	46.6	3.9	2011	6	5256770-6	Patent No. 5256770
30	46.6	3.9	2011	6	5256770-6	Patent No. 5256770
31	46.6	3.9	34953	4	US-09-902-540-1263	Sequence 1263, Ap
32	45	3.7	505	4	US-09-621-976-15639	Sequence 15639, A
33	44.6	3.7	1491	4	US-09-902-540-2350	Sequence 2350, Ap
34	44.6	3.7	13751	4	US-09-902-540-1099	Sequence 1099, Ap
35	44.2	3.7	840	4	US-09-902-540-56	Sequence 56, Appli
36	44.2	3.7	1164	1	US-07-640-476-6	Sequence 6, Appli
37	43.6	3.6	1251	4	US-09-902-540-7778	Sequence 7778, Ap
38	43.6	3.6	12898	4	US-09-902-540-1000	Sequence 1000, Ap
39	42.8	3.6	984	4	US-09-489-039A-1470	Sequence 1470, Ap
40	42.8	3.6	1035	4	US-09-902-540-8589	Sequence 8589, Ap
41	42.8	3.6	1722	4	US-09-902-540-9668	Sequence 9668, Ap
42	42.8	3.6	6682	4	US-09-902-540-906	Sequence 906, App
43	42.8	3.6	14555	4	US-09-902-540-1096	Sequence 1096, Ap
44	42.8	3.6	28804	2	US-08-592-874-1	Sequence 1, Appli
45	42.8	3.6	28804	3	US-09-096-942-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-959-897-1
; Sequence 1, Application US/09959897
; Patent No. 6730480
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMELE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/09/959,897
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 1205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)..(1184)
; OTHER INFORMATION:
US-09-959-897-1

Query Match	100.0%;	Score 1205;	DB 4;	Length 1205;
Best Local Similarity	100.0%;	Pred. No. 5.2e-282;	Mismatches 0;	Gaps 0;
Matches 1205;	Conservative 0;			
QY	1	GAATTCGGCAGGAGCGCGGTCGAGTTATGGATCAGCGCGCGCCCGCGGGCG	60	
Db	1	GAATTCGGCAGGAGCGCGGTCGAGTTATGGATCAGCGCGCGCCCGCGGGCG	60	
QY	61	TGCTCCCGCGCCCTGTCGCGGTGCTGCTGCTGAACCCCGCGCGCGCAAGG	120	
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QY	181	CGCTGATGCTCACTGAGCGCGGAACACCGCGCGGAGCTGGTGGTTCGAGGAGCTGG	240	

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Db 181 CGCTGATGCTCACTGAGCGGCGAACCACGCGCGGAGCTGGTGGGTCGAGAGAGCTGG 240
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Db 361 CAGGCTCTGGCAACCGGCTGGCAGCTTCTTGAACCAATTATGCTGGCTATGACGAGGTCA 420
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QY 481 TGAACCTGCTGCTCTGACACAGGCTTGGGGCTGGGCTCTTCTCTGTGCTCAGCCTGG 540
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RESULT 2

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US-09-949-016-1155
; Sequence 1155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1155
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1155
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Query Match 96.5%; Score 1162.6; DB 4; Length 1783;
Best Local Similarity 98.4%; Pred. No. 1.1e-271;
Matches 1174; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db 371 CGCGGCGCTGCGCGGCTGCTGTGCTGAACCCGCGCGGGCGGCAAGGCAAGCCTTGC 430
QY 127 AGCTCTTCCGAGTCAGTGCAGCCCTTTTGGCTGAGGCTGAATCTCTTACGCTGA 186
Db 431 AGCTCTTCCGAGTCAGTGCAGCCCTTTTGGCTGAGGCTGAATCTCTTACGCTGA 490
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QY 487 TGCTGTCTGTGACACGCGCTTCCGGGCTGCGGCTTCTCTGTGCTCAGCTGCGCTGGG 546
Db 791 TGCTGTCTGTGACACGCGCTTCCGGGCTGCGGCTTCTCTGTGCTCAGCTGCGCTGGG 850
QY 547 GCTTCATTGCTGATGTGGACCTAGAGAGTGAAGATTCGGCGGTCTGGGGAGATGCGCT 606
Db 851 GCTTCATTGCTGATGTGGACCTAGAGAGTGAAGATTCGGCGGTCTGGGGAGATGCGCT 910
QY 607 TCACCTGCGGCACTTTCCTGGGCTGCGGCTTGGCAGCTTACCGCGGCGGCTGCGCTT 666
Db 911 TCACCTGCGGCACTTTCCTGGGCTGCGGCTTGGCAGCTTACCGCGGCGGCTGCGCTT 970
QY 667 ACCTCCCTGTAGGAAGAGTGGGTTCCCAAGACACCTGCTCCCGCTTGTGCTCCAGCAGG 726
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Db 971 ACCTCCCTGTAGGAAGAGTGGTTCCAGACACCTGCTCCCTGCTGGTCCAGCAGG 1030
QY 727 GCCCGGTAGATGCACACCTTTGTCACCTGGAGAGCCAGTGCCTCTCACTGACAGTGG 786
Db 1031 GCCCGGTAGATGCACACCTTTGTCACCTGGAGAGCCAGTGCCTCTCACTGACAGTGG 1090
QY 787 TGCCCGAGAGAGACTTTGCTAGTCTGGCACTGCTGCACCTCGACCTGGGCACTGAGA 846
Db 1091 TGCCCGAGAGAGACTTTGCTAGTCTGGCACTGCTGCACCTCGACCTGGGCACTGAGA 1150
QY 847 TGTTTGTCTGACCCATGGCCGCTGTGCAGCTGGCGTCAATGATCTGTTCTACGTGCGGG 906
Db 1151 TGTTTGTCTGACCCATGGCCGCTGTGCAGCTGGCGTCAATGATCTGTTCTACGTGCGGG 1210
QY 907 CGGAGTGTCTCGTGCCATGCTGCTGCGCTTTCTTGCCCATGAGAGAGGCGAGCATA 966
Db 1211 CGGAGTGTCTCGTGCCATGCTGCTGCGCTTTCTTGCCCATGAGAGAGGCGAGCATA 1270
QY 967 TCGAGTATGAATGCCCTTACTTGGTATATGTCGCGGTGTCGCTTCCGCTTGGAGCCCA 1026
Db 1271 TCGAGTATGAATGCCCTTACTTGGTATATGTCGCGGTGTCGCTTCCGCTTGGAGCCCA 1330
QY 1027 AGGATGGGAAAGTATGTTTGCAGTGGATGGGAAATTCATGTTAGCCAGGCGCTGCAGG 1086
Db 1331 AGGATGGGAAAGTATGTTTGCAGTGGATGGGAAATTCATGTTAGCCAGGCGCTGCAGG 1390
QY 1087 GCCAGTGCACCCAACTACTTCTGATGCTGAGCGTTGCGTGGAGAGCCCGCCAGCT 1146
Db 1391 GCCAGTGCACCCAACTACTTCTGATGCTGAGCGTTGCGTGGAGAGCCCGCCAGCT 1450
QY 1147 GGAAGCCCGACGAGATGCCACCGCCAGAGAGCCCTTATGATCTAGAGTCGAC 1199
Db 1451 GGAAGCCCGACGAGATGCCACCGCCAGAGAGCCCTTATGATCTAGAGTCGAC 1503

RESULT 3

US-09-205-258-90
; Sequence 90, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE


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Db 421 TTGCTGTGCGCGCGCTGCTGTCAACCATGAACCTGCTGTCTCTGCACACGCGCTTCGCGG 480
QY 513 CTGCGGCTTTCTCTGTGTCTAGACCTGGCTGGGCTTCATTGCTGATGTGACCTAGAG 572
Db 481 CTGCGGCTTTCTCTGTGTCTAGACCTGGCTGGGCTTCATTGCTGATGTGACCTAGAG 540
QY 573 AGTGAGAGTATCGGCGCTCTGGGAGATGCGCTTCACTCTGGGCACTTTCCTGGCTCTG 632
Db 541 AGTGAGAGTATCGGCGCTCTGGGAGATGCGCTTCACTCTGGGCACTTTCCTGGCTCTG 600
QY 633 GCAGCCTTTCGCACTTACCGCGCGCACTGGCTTACCTCCCTGTAGGAAGAGTGGTTCC 692
Db 601 GCAGCCTTCGCACTTACCGCGCGCACTGGCTTACCTCCCTGTAGGAAGAGTGGTTCC 660
QY 693 AAGACACCTGCTCCCGCTTGTGTCTCAGCAGGCGCGGTAGATGCAACCTTGTGCCA 752
Db 661 AAGACACCTGCTCCCGCTTGTGTCTCAGCAGGCGCGGTAGATGCAACCTTGTGCCA 720
QY 753 CTGGAGGACCACTGCTCTCACTGGACAGTGGTGGCGCGAGGACCTTTCCTGTAGTC 812
Db 721 CTGGAGGACCACTGCTCTCACTGGACAGTGGTGGCGCGAGGACCTTTCCTGTAGTC 780
QY 813 CTGGCACTGCTGCACCTCGCACCTGGGCACTGAGATGTTTGTGCAACCCATGGGCGCTGT 872
Db 781 CTGGCACTGCTGCACCTCGCACCTGGGCACTGAGATGTTTGTGCAACCCATGGGCGCTGT 840
QY 873 GCAGCTGGCGTCAATGATCTGTTCTACGTGGCGGCGGAGTGTCTGTGCCATGCTGCTG 932
Db 841 GCAGCTGGCGTCAATGATCTGTTCTACGTGGCGGCGGAGTGTCTGTGCCATGCTGCTG 900
QY 933 CGCCTCTCTCGCCATGAGAGGCGCAGCATATGAGTATGAATGCCCTACTTTGGTA 992
Db 901 CGCCTCTCTCGCCATGAGAGGCGCAGCATATGAGTATGAATGCCCTACTTTGGTA 960
QY 993 TATGTCCCGTGTGCTGCTTCCGCTTGGAGCCCAAGGATGGGAAGATGTTTGCAGTG 1052
Db 961 TATGTCCCGTGTGCTGCTTCCGCTTGGAGCCCAAGGATGGGAAGATGTTTGCAGTG 1020
QY 1053 GATGGGAATGATGTTAGCGAGGCGGTGCGAGGCGGCGGAGTGTCTGTGCCATGCTGCTG 1112
Db 1021 GATGGGAATGATGTTAGCGAGGCGGTGCGAGGCGGCGGAGTGTCTGTGCCATGCTGCTG 1080
QY 1113 ATGGTCAGCGTGTGCTGAGGCGGCGGCGGCGGAGTGTGAGCGGCGGAGTGTGAGCGGCA 1172
Db 1081 ATGGTCAGCGTGTGCTGAGGCGGCGGCGGCGGAGTGTGAGCGGCGGAGTGTGAGCGGCA 1140
QY 1173 GAAGAGCCCTTATGA 1187
Db 1141 GAAGAGCCCTTATGA 1155

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RESULT 5
US-09-949-016-3940
; Sequence 3940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3940
; LENGTH: 1764
; TYPE: DNA

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i ORGANISM: Human
US-09-949-016-3940

Query Match      89.7%; Score 1081.4; DB 4; Length 1764;
Best Local Similarity 95.8%; Pred. No. 4.6e-252; Indels 4; Gaps 2;
Matches 1133; Conservative 0; Mismatches 46;

QY 7 GGCACAGAGAGCCGCGGCTCGAGGTTATGGATCCAGCGGCGGCGGCGGCGGCGGCTGCTCC 66
Db 311 GGCAGCGGAGCGCGGCTCGAGGTTATGGATCCAGCAGGCGGCGGCGGCGGCGGCTGCTC 370
QY 67 CGCGGCTTGC CGCGCTGTGTGTCTGCTGAACCCCGCGGCGGCGGCGGCGGCGGCGGCTTGC 126
Db 371 CGCGGCTTGC CGCGCTGTGTGTCTGCTGAACCCCGCGGCGGCGGCGGCGGCGGCGGCTTGC 426
QY 127 AGCTCTTCGCGAGTCACTGTGAGGCGGCTTTCGCTGAGGCTGAGGCTGAGGCTGAGGCTG 186
Db 427 AGCTCTTCGCGAGTCACTGTGAGGCGGCTTTCGCTGAGGCTGAGGCTGAGGCTGAGGCTG 486
QY 187 TGCTCACTGAGCGGCGGAAACCAACCGCGGCGGAGCTGGTGGCTCGAGGAGCTGGGCGGCT 246
Db 487 TGCTCACTGAGCGGCGGAAACCAACCGCGGCGGAGCTGGTGGCTCGAGGAGCTGGGCGGCT 546
QY 247 GGGACGCTTGTGTGTCTGTCTGAGAGCGGCTGTATGCAAGAGTGTGTGAACGGGCTCA 306
Db 547 AGGACGCTTGTGTGTCTGTCTGAGAGCGGCTGTATGCAAGAGTGTGTGAACGGGCTCA 606
QY 307 TGGAGCGGCTGACTGGGAGACCGCCATCCAGAGCGGCTGTGTAGCTTCCAGCAGGCT 366
Db 607 TGGAGCGGCTGACTGGGAGACCGCCATCCAGAGCGGCTGTGTAGCTTCCAGCAGGCT 666
QY 367 CTGGCAACGCGCTGGCAGCTTCTTTGAACCAATATGCTGGCTATGAGCAGGTCACCAATG 426
Db 667 CTGGCAACGCGCTGGCAGCTTCTTTGAACCAATATGCTGGCTATGAGCAGGTCACCAATG 726
QY 427 AAGACCTCTGTACCAACTGACGCTATGCTGTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGT 486
Db 727 AAGACCTCTGTACCAACTGACGCTATGCTGTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGT 786
QY 487 TGCTGTCTGACACGCGCTTGGGCGCTGCGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 546
Db 787 TGCTGTCTGACACGCGCTTGGGCGCTGCGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 846
QY 547 GCTTCATTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606
Db 847 GCTTCATTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 906
QY 607 TCACTCTGGGCACTTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
Db 907 TCACTCTGGGCACTTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 966
QY 667 ACCTCCCTGTAGAGAGAGTGGGTTCCAGACACCTGCTCCCGGCTGTGTGTGTGTGTGTGTGT 726
Db 967 ACCTCCCTGTAGAGAGAGTGGGTTCCAGACACCTGCTCCCGGCTGTGTGTGTGTGTGTGTGT 1026
QY 727 GCCCGGTAGATGACACACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
Db 1027 GCCCGGTAGATGACACACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1086
QY 787 TGCCTCCGACGAGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 846
Db 1087 TGCCTCCGACGAGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1146
QY 847 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 906
Db 1147 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1206
QY 907 CGGGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 966
Db 1207 CGGGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1266
QY 967 TGGAGTATGAATGCCCTTATGTTGGTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026

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Db 1267 TGGAGTATGAATGCCCTACTTTGGTATATGTGTGCCCGTGGTCCGCTTCCGCTTGGAGCCCA 1326
QY 1027 AGGATGGGAAAGTATGTTTGCAGTGGATGGGAAATGATGGTTAGCAGAGCCGTGCGAGG 1086
Db 1327 AGGATGGGAAAGTGTGTTTGCAGTGGATGGGAAATGATGGTTAGCAGAGCCGTGCGAGG 1386
QY 1087 GCCAGGTGCACCAACTACTTCTGGATGGTTCAGCGGTTGGTGGAGCCCGCCCGCCAGCT 1146
Db 1387 GCCAGGTGCACCAACTACTTCTGGATGGTTCAGCGGTTGGTGGAGCCCGCCCGCCAGCT 1446
QY 1147 GGAAGCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1189
Db 1447 GGAAGCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGACC 1489

RESULT 6
US-09-949-016-12897
; Sequence 12897, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12897
; LENGTH: 7195
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12897

Query Match 64.3%; Score 774.4; DB 4; Length 7195;
Best Local Similarity 99.2%; Pred. No. 1.3e-177;
Matches 778; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 406 GCTATGAGCAGGTCAACCAATGAAGACCTCTGACCAACTGACGCTATTGCTGTGCCGCC 465
Db 4140 GCTATGAGCAGGTCAACCAATGAAGACCTCTGACCAACTGACGCTATTGCTGTGCCGCC 4199
QY 466 GGCTGCTGTCAACCATGAACCTGCTGTCTGACACAGGCTTCGGGGCTGCGCCTCTTCT 525
Db 4200 GGCTGCTGTCAACCATGAACCTGCTGTCTGACACAGGCTTCGGGGCTGCGCCTCTTCT 4259
QY 526 CTGTGCTCAGCCTGGCGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATC 585
Db 4260 CTGTGCTCAGCCTGGCGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATC 4319
QY 586 GCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTTCGGAGCCTTGGCGCA 645
Db 4320 GCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTTCGGAGCCTTGGCGCA 4379
QY 646 CTTACCGGGCGGACTGGCTTACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCT 705
Db 4380 CTTACCGGGCGGACTGGCTTACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCT 4439
QY 706 CCCCCGTTGTGCTCAGCAGGCGCGGTAGATGCAACCTTGTGCACTGGAGGAGCCAG 765
Db 4440 CCCCCGTTGTGCTCAGCAGGCGCGGTAGATGCAACCTTGTGCACTGGAGGAGCCAG 4499
QY 766 TGCCCTCTCACTGACAGTGTGTCGCGCCGACGAGGACTTTGTGCTAGTCTGGCACTGTGCG 825
Db 4500 TGCCCTCTCACTGACAGTGTGTCGCGCCGACGAGGACTTTGTGCTAGTCTGGCACTGTGCG 4559
QY 826 ACTCGCACTGGGAGTGAGATGTTTGTGCAACCCATGGGCGGCTGTGACGTGCGTCA 885
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Db 4560 ACTCGCACTGGGAGTGAGATGTTTGTGCACCATGGGCCGCTGTGCAGCTGCGGTCA 4619
QY 886 TGCATCTGTTCTACGTGCGGCGGAGTGTCTCGTGCATGCTCTGCGCCTCTTTCCTGG 945
Db 4620 TGCATCTGTTCTACGTGCGGCGGAGTGTCTCGTGCATGCTCTGCGCCTCTTTCCTGG 4679
QY 946 CCATGAGAGAGGCGAGCATATGAGTATGAATGCCCTACTTGGTATATGTGCCCGTGG 1005
Db 4680 CCATGAGAGAGGCGAGCATATGAGTATGAATGCCCTACTTGGTATATGTGCCCGTGG 4739
QY 1006 TCGCCTTCCGCTTGCAGCCCAAGATGGGAAAGTATGTTTGCAGTGTGATGGGAATTGA 1065
Db 4740 TCGCCTTCCGCTTGCAGCCCAAGATGGGAAAGTATGTTTGCAGTGTGATGGGAATTGA 4799
QY 1066 TGGTTAGCGAGGCGCTGCAGGCCAGGTGCACCCAAACTACTTCTGGATGTCAGCGGTT 1125
Db 4800 TGGTTAGCGAGGCGCTGCAGGCCAGGTGCACCCAAACTACTTCTGGATGTCAGCGGTT 4859
QY 1126 GCGTGGAGCCCCCGCCAGCTGGGAAGCCCGAGCAGATGCCACCGCAGAGGCGCTTAT 1185
Db 4860 GCGTGGAGCCCCCGCCAGCTGGGAAGCCCGAGCAGATGCCACCGCAGAGGCGCTTAT 4919
QY 1186 GATC 1189
Db 4920 GACC 4923

RESULT 7
US-09-949-016-15682
; Sequence 15682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15682
; LENGTH: 7198
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15682

Query Match 64.3%; Score 774.4; DB 4; Length 7198;
Best Local Similarity 99.2%; Pred. No. 1.3e-177;
Matches 778; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 406 GCTATGAGCAGGTCAACCAATGAAGACCTCTGACCAACTGACGCTATTGCTGTGCCGCC 465
Db 4140 GCTATGAGCAGGTCAACCAATGAAGACCTCTGACCAACTGACGCTATTGCTGTGCCGCC 4199
QY 466 GGCTGCTGTCAACCATGAACCTGCTGTCTGACACAGGCTTCGGGGCTGCGCCTCTTCT 525
Db 4200 GGCTGCTGTCAACCATGAACCTGCTGTCTGACACAGGCTTCGGGGCTGCGCCTCTTCT 4259
QY 526 CTGTGCTCAGCCTGGCGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATC 585
Db 4260 CTGTGCTCAGCCTGGCGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATC 4319
QY 586 GCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTTCGGAGCCTTGGCGCA 645
Db 4320 GCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTTCGGAGCCTTGGCGCA 4379
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Db      1138 GAAGAACCATRA 1149

RESULT 9
US-09-949-016-40620
; Sequence 40620, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40620
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40620

Query Match      40.8%; Score 491.4; DB 4; Length 601;
Best Local Similarity 99.4%; Pred. No. 1.9e-109;
Matches 492; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      695 GACACCTGCTCCCGCTTGTGTCACAGAGCCCGGTAGATGACACACTTTGTGCCACT 754
Db      1 GACACCTGCTCCCGCTTGTGTCACAGAGCCCGGTAGATGACACACTTTGTGCCACT 60

Qy      755 GGAGGAGCAGTGCCCTCTCACTGGACAGTGGTCCCGACGAGACTTTGTGTAGTCT 814
Db      61 GGAGGAGCAGTGCCCTCTCACTGGACAGTGGTCCCGACGAGACTTTGTGTAGTCT 120

Qy      815 GGCACCTGTCACCTCGCACCTGGGACGTGAGATGTTTCTGCACCCATGGGCCGCTGTC 874
Db      121 GGCACCTGTCACCTCGCACCTGGGACGTGAGATGTTTCTGCACCCATGGGCCGCTGTC 180

Qy      875 AGCTGGGCTCATGATCTGTTCTACGTGGGCGGGAGTGTCTCGTGCATGCTGCTGCG 934
Db      181 AGCTGGGCTCATGATCTGTTCTACGTGGGCGGGAGTGTCTCGTGCATGCTGCTGCG 240

Qy      935 CCTCTTCTGGCCATGGAGAGGCGGAGCATATGAGTATGAATGCCCTACTTTGGTATA 994
Db      241 CCTCTTCTGGCCATGGAGAGGCGGAGCATATGAGTATGAATGCCCTACTTTGGTATA 300

Qy      995 TGTGCCCGTGTGCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA 1054
Db      301 TGTGCCCGTGTGCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA 360

Qy      1055 TGGGGAATTGATGTTAGCGAGCCCGTGCAGGCGCGGTGACCCCAAACTACTTCTGGAT 1114
Db      361 TGGGGAATTGATGTTAGCGAGCCCGTGCAGGCGCGGTGACCCCAAACTACTTCTGGAT 420

Qy      1115 GGTACAGCGTTGCGTGGAGCCCGCCGAGCTGGAAGCCCGCAGAGATGCCACGCCAGA 1174
Db      421 GGTACAGCGTTGCGTGGAGCCCGCCGAGCTGGAAGCCCGCAGAGATGCCACGCCAGA 480

Qy      1175 AGAGCCCTTATGATC 1189
Db      481 AGAGCCCTTATGACC 495

RESULT 10
US-09-949-016-139382
; Sequence 139382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139382
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-139382

Query Match      40.8%; Score 491.4; DB 4; Length 601;
Best Local Similarity 99.4%; Pred. No. 1.9e-109;
Matches 492; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      695 GACACCTGCTCCCGCTTGTGTCACAGAGCCCGGTAGATGACACACTTTGTGCCACT 754
Db      1 GACACCTGCTCCCGCTTGTGTCACAGAGCCCGGTAGATGACACACTTTGTGCCACT 60

Qy      755 GGAGGAGCAGTGCCCTCTCACTGGACAGTGGTCCCGACGAGACTTTGTGTAGTCT 814
Db      61 GGAGGAGCAGTGCCCTCTCACTGGACAGTGGTCCCGACGAGACTTTGTGTAGTCT 120

Qy      815 GGCACCTGTCACCTCGCACCTGGGACGTGAGATGTTTCTGCACCCATGGGCCGCTGTC 874
Db      121 GGCACCTGTCACCTCGCACCTGGGACGTGAGATGTTTCTGCACCCATGGGCCGCTGTC 180

Qy      875 AGCTGGGCTCATGATCTGTTCTACGTGGGCGGGAGTGTCTCGTGCATGCTGCTGCG 934
Db      181 AGCTGGGCTCATGATCTGTTCTACGTGGGCGGGAGTGTCTCGTGCATGCTGCTGCG 240

Qy      935 CCTCTTCTGGCCATGGAGAGGCGGAGCATATGAGTATGAATGCCCTACTTTGGTATA 994
Db      241 CCTCTTCTGGCCATGGAGAGGCGGAGCATATGAGTATGAATGCCCTACTTTGGTATA 300

Qy      995 TGTGCCCGTGTGCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA 1054
Db      301 TGTGCCCGTGTGCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA 360

Qy      1055 TGGGGAATTGATGTTAGCGAGCCCGTGCAGGCGCGGTGACCCCAAACTACTTCTGGAT 1114
Db      361 TGGGGAATTGATGTTAGCGAGCCCGTGCAGGCGCGGTGACCCCAAACTACTTCTGGAT 420

Qy      1115 GGTACAGCGTTGCGTGGAGCCCGCCGAGCTGGAAGCCCGCAGAGATGCCACGCCAGA 1174
Db      421 GGTACAGCGTTGCGTGGAGCCCGCCGAGCTGGAAGCCCGCAGAGATGCCACGCCAGA 480

Qy      1175 AGAGCCCTTATGATC 1189
Db      481 AGAGCCCTTATGACC 495

RESULT 11
US-09-970-516-3
; Sequence 3, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1857)
; OTHER INFORMATION:
US-09-970-516-3

Query Match      21.4%; Score 258; DB 4; Length 1857;
Best Local Similarity 63.3%; Pred. No. 7.8e-53;
Matches 396; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 50 CCCCCGGGCGTGTCTCCCGCGCCCTGCGCGTGTGCTGTGCTGTGAACCCCGCGGGCG 109
DB 408 CACCCCTGACCTGCTACCTCGCGCGCGCGTGTCTTATTGGTCAATCCCTTTGGGGG 467
QY 110 CAAAGGCAAGGCTTTCAGCTCTTCGGAGTCACTGAGCGCCCTTTGGCTGAGGCTGA 169
DB 468 TCGGGGCTTGGCTTGGCTGTGAGTGTGAAGAACACAGCTGTCCCATGATCTCTGAAGCTGG 527
QY 170 AATCTCTTCAAGCTGATCTCACTGAGCGCGGGAACACAGCGCGGAGCTGTGGGTC 229
DB 528 GCTGTCTTCAACCTCATCCAGACAGACAGAACACAGCGCGGAGCTGTCCAGGG 587
QY 230 GGAGGAGCTGGGCGGCTGCGAGCGCTCTGGTGTGATGTCTGGAGAGCGGCTGATGCACGA 289
DB 588 GCTGAGCTGTAGTGTGAGTGGATGGCATGCTCAGCGTCTCGGAGAGCGGCTGCTCCATGA 647
QY 290 GGTGTGTAAACGGGCTCATGAGCGGCTGACTGGGAGACCGGCATCCAGAACGCCCTGTG 349
DB 648 GGTGTGTAAACGGGCTCTAGATCGCCCTGACTGGGAGGAGCTGTGAAGATGCTGTGGG 707
QY 350 TAGCTTCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCTTGAACCATTTATGTGGCTA 409
DB 708 CATCTCTCCCTGCGGCTCGGGCAACGCGTGGCGGAGCAGTGAACACAGCAGGGGAT 767
QY 410 TGAGCAGGTCAACCAATGAAGACCTCTGACCAACTCAGCGTATTTCTGTCCCGCGGCT 469
DB 768 TGAGCAGGCTGGGCTGACCTGTGTGCTCACTGCTCACTGCTGTGCGGGGTGG 827
QY 470 GCTGTCAACCAATGAAGCTGTCTCTGCAACGCGTGTGGGCTGCGGCTCTTCTCTGT 529
DB 828 TGSCCACCCTGACCTGCTCTCCGTGACGCTGGGCTCGGGCTCCCGCTGTTTCTCTT 887
QY 530 GCTCAGCTGGCTGGGCTTCAATGCTGTGAGTGGACCTAGAGAGTGAAGATATCGGCG 589
DB 888 CTTGTCTGTGGCTTGGGCTTCTGTGTGATGTGGATATCCAGAGCAGCGCTTCAGGGC 947
QY 590 TCTGGGGAGATGGCTTCACTTGGGCACTTTCTCGCTGTGGCAGCTTGGGCACTTA 649
DB 948 CTTGGGAGTGGCCGCTTCAACTGGGCAAGGCTGTGGGCTCGCCACTGCACACTGA 1007
QY 650 CCGCGGCGGACTGGCTTACCTCCCTG 675
DB 1008 CCGGAGGCTCTCTCTACCTCCCG 1033
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RESULT 12
US-09-817-676A-13
; Sequence 13, Application US/09817676A
; Patent No. 6800470
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Kohama, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; TITLE OF INVENTION: Expression and Methods of Use Thereof
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT FILING DATE: 2001-03-26

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; PRIOR APPLICATION NUMBER: US 60/194,318
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1860)
; PUBLICATION INFORMATION:
; TITLE: Molecular cloning and functional characterization of a
; TITLE: novel mammalian sphingosine kinase type 2 isoform
; JOURNAL: J. Biol. Chem.
; VOLUME: 275
; ISSUE: 26
; PAGES: 19513-19520
; DATE: 2000-06-30
; DATABASE ACCESSION NUMBER: AF245447
; DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-13
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Query Match      21.4%; Score 258; DB 4; Length 2380;
Best Local Similarity 63.3%; Pred. No. 8.4e-53;
Matches 396; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 50 CCCCCGGGCGTGTCTCCCGCGCCCTGCGCGTGTGCTGTGCTGTGAACCCCGCGGGCG 109
DB 414 CACCCCTGACCTGCTACCTCGCGCGCGGTTGCTTATTGGTCAATCCCTTTGGGGG 473
QY 110 CAAAGGCAAGGCTTTCAGCTCTTCCGAGTCACTGAGCGGCGGAAACACCGCGGAGCTGTGAGGCTGA 169
DB 474 TCGGGGCTTGGCTGTGAGTGTGAAGAACCACTGCTTCCCATGATCTCTGAAGCTGG 533
QY 170 AATCTCTTCAAGCTGATGCTCACTGAGCGGCGGAAACACCGCGGAGAGCTGTGGGTC 229
DB 534 GCTGTCTTCAACCTCATCCAGACAGACAGAACACACCGCGCGGAGCTGTCCAGGG 593
QY 230 GGAGAGCTGGGCGGCTGCGAGCGCTCTGGTGTGATGTCTGAGAGCGGCTGATGCACGA 289
DB 594 GCTGAGCTGTAGTGTGGGATGGCATGCTACGGTCTCGGAGAGCGGCTGCTCCATGA 653
QY 290 GGTGTGTAAACGGGCTCATGGAGCGGCTGACTGGGAGACCGGCATCCAGAACGCCCTGTG 349
DB 654 GGTGTGTAAACGGGCTCTAGATCGCCCTGACTGGGAGGAGCTGTGAAGATGCTGTGGG 713
QY 350 TAGCCTTCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCTTGAACCATTTATGTGGCTA 409
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QY 410 TGAGCAGGTCAACCAATGAAGACCTCTCTGACCACTGACGCTATTGCTGTGGCGCGGCT 469
DB 774 TGAGCAGGCTTGGGCTGCGACCTGTGCTCACTGCTCACTGCTGTGGGCGGGTGG 833
QY 470 GCTGTCAACCATGAAGCTGCTCTCTGCAACGCGCTTGGGCGCTCGGCTCTTCTCTGT 529
DB 834 TGGCCACCCACTGAGCTGCTCTCTCGTGTGAGCTGGGCTCGGGCTCCCGCTGTTTCTCTT 893
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QY 650 CCGGCGCGGACTGGCTTACCTCCCTG 675
DB 1014 CCGCGAGCCTCTCTCTACCTCCCG 1039
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RESULT 13


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US-09-270-767-12677
; Sequence 12677, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12677
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12677

Query Match          6.5%; Score 78.6; DB 4; Length 1012;
Best Local Similarity 55.8%; Pred. No. 1.7e-09;
Matches 150; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 68 GCGGCCCTGCCCGTGTGCTGTGAACCGCGCGCGCGCAAGGGCAAGGCCTTGCA 127
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QY 128 GCTCTTCGGAGTCAGTGCAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGAT 187
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 804 GGTCTTCAACATGCACGTGACCGCGTGTCAATGAGCGCGAGTGCCCTACGACCTGTA 863
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 GCTCACTGAGCGCGGAACACGCGCGGAGCTGGTGGTGGAGAGCTGGGCGGCTG 247
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 864 TGTAAACCAAGCATTCGAATTTGCCATCGAGTTCTTGAGCACCAGGTGCTGGACGCTG 923
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QY 248 GGACGCTCTGGTGTGTCATGCTGGAGACGGGCTGATGCAAGAGGTGTGAAACGGGCTCAT 307
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QY 924 GTGCTGCGTGTGGTGTGTCGGCGGAGACGGTCTCTTCCACGAGATAGTCAATGGACTGCT 983
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QY 308 GGAGCGGCTGACTGGGAGACCGCCATCC 336
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QY 984 GCAGCGCCAGGACTGGGCCCCACGTCCTGC 1012
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 1205
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Searched: 6054689 seqs, 3103772919 residues

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1168.6	97.0	2137	20	Sequence 1, Appli
3	1168.2	96.9	1799	16	Sequence 225, App
4	1162.6	96.5	1783	20	Sequence 25, Appl
5	1149.4	95.4	1533	10	Sequence 721, App
6	1149.4	95.4	1533	14	Sequence 90, Appl
7	1149.4	95.4	1533	14	Sequence 90, Appl
					Sequence 90, Appl

8	1147	95.2	1155	9	US-09-970-516-1	Sequence 1, Appli
9	1147	95.2	1155	18	US-10-619-344-1	Sequence 1, Appli
10	1142.4	94.8	1152	17	US-10-348-052-22	Sequence 22, Appl
11	1142.4	94.8	1152	19	US-10-622-011-22	Sequence 22, Appl
12	1141.4	94.7	1600	9	US-09-784-810A-1	Sequence 1, Appli
13	1141.4	94.7	1600	22	US-10-876-281-1	Sequence 1, Appli
14	1140.4	94.6	1562	17	US-10-264-237-1180	Sequence 1180, Ap
15	1140.4	94.6	1869	19	US-10-715-117-1	Sequence 1, Appli
16	1140.4	94.6	1197	19	US-10-715-117-3	Sequence 3, Appli
17	1115.2	92.5	2551	20	US-10-723-860-5339	Sequence 5339, Ap
18	770.4	63.9	1759	9	US-09-784-810A-3	Sequence 3, Appli
19	770.4	63.9	1759	22	US-10-876-281-3	Sequence 3, Appli
20	760	63.1	1149	9	US-09-970-516-5	Sequence 5, Appli
21	760	63.1	1149	18	US-10-619-344-5	Sequence 9248, Ap
22	292.6	24.3	480	9	US-09-783-590-9248	Sequence 9248, Ap
23	258	21.4	1857	9	US-09-970-516-3	Sequence 3, Appli
24	258	21.4	1857	18	US-10-619-344-3	Sequence 3, Appli
25	258	21.4	2380	9	US-09-817-676A-13	Sequence 13, Appl
26	258	21.4	2380	16	US-10-354-358-77	Sequence 77, Appl
27	258	21.4	2380	19	US-10-283-975A-515	Sequence 515, App
28	258	21.4	2380	20	US-10-830-677-13	Sequence 13, Appl
29	258	21.4	2380	20	US-10-737-450-139	Sequence 139, App
30	245.2	20.3	2698	9	US-09-817-676A-11	Sequence 11, Appl
31	245.2	20.3	2698	20	US-10-830-677-11	Sequence 11, Appl
32	213.6	17.7	310	20	US-10-425-115-15523	Sequence 15523, A
33	195.8	16.2	199	9	US-09-796-692-2905	Sequence 2905, Ap
34	195.8	16.2	199	14	US-10-040-862-2905	Sequence 2905, Ap
35	195.8	16.2	199	17	US-10-057-475B-2905	Sequence 2905, Ap
36	195.8	16.2	199	17	US-10-154-884B-2905	Sequence 2905, Ap
37	195.8	16.2	199	19	US-10-764-324-2905	Sequence 2905, Ap
38	191.4	15.9	296	9	US-09-777-564-658	Sequence 658, App
39	191.4	15.9	296	14	US-10-015-219-658	Sequence 658, App
40	176.8	14.7	801	18	US-10-296-115-69	Sequence 69, Appl
41	159.2	13.2	1172	19	US-10-283-975A-584	Sequence 584, App
42	119.2	9.9	394	9	US-09-954-456-1756	Sequence 1756, Ap
43	119.2	9.9	394	21	US-10-843-641A-4783	Sequence 4783, Ap
44	114.4	9.5	1521	18	US-10-168-582-23	Sequence 23, Appl
45	111.2	9.2	832	16	US-10-029-386-20952	Sequence 20952, A

ALIGNMENTS

RESULT 1
US-10-642-289-1
; Sequence 1, Application US/10642289
; Publication No. US20040132053A1
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/10/642,289
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/959,897
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Qy	427	AAGACCTCTGACCAACTGCA	CGCTATTGCTGTGCGCGGCTGCTGCA	CCCAATGAACC	486
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Qy	487	TGCTGTCTCTGCACACGGCT	TCGGGGCTTGGGCTCTTCTGTGCTCAGCTGAGCCTGGCTGGG	546	
Db	1169	TGCTGTCTCTGCACACGGCT	TCGGGGCTTGGGCTCTTCTGTGCTCAGCTTGGCCTGGG	1228	
Qy	547	GCTTCACTGCTGATGTGGAC	CTTAGAGAGTGAGAAGTATCGGCGCTCTGGGGGAGATGCGCT	606	
Db	1229	GCTTCACTGCTGATGTGGAC	CTTAGAGAGTGAGAAGTATCGGCGCTCTGGGGGAGATGCGCT	1288	
Qy	607	TCACCTCGGGCACTTTCCT	GTGCGTCTGGCAGCTTGGGCACTTACCGCGGCGCAGCTGGCTT	666	
Db	1289	TCACCTCGGGCACTTTCCT	GTGCGTCTGGCAGCGCTGCGCACTTACCGCGCGCAGCTGGCTT	1348	
Qy	667	ACCTCCCTCTAGGAGAGTGG	GTTCACAGACACTTGCCTCCCGCTGTGTGCTCAGCAGG	726	
Db	1349	ACCTCCCTCTAGGAGAGTGG	GTTCACAGACACTTGCCTCCCGCTGTGTGCTCAGCAGG	1408	
Qy	727	GCCCGGTAGATGCACACCT	TGTGTGCCACTGGAGGAGCCAGTGGCCCTCTCACTGGACAGTGG	786	
Db	1409	GCCCGGTAGATGCACACCT	TGTGTGCCACTGGAGGAGCCAGTGGCCCTCTCACTGGACAGTGG	1468	
Qy	787	TGCCCGACGAGGACTTTGT	GTGCTAGTCTGGCACTGCGCACTGCGCACTGGGCGAGTGAGA	846	
Db	1469	TGCCCGACGAGGACTTTGT	GTGCTAGTCTGGCACTGCGCACTGCGCACTGGGCGAGTGAGA	1528	
Qy	847	TGTTTCTGCACCCATGGGCG	CGCTGTGCAGCTGGGCTCATGCTTGTCTACGTGCGGG	906	
Db	1529	TGTTTCTGCACCCATGGGCG	CGCTGTGCAGCTGGGCTCATGCTTGTCTACGTGCGGG	1588	
Qy	907	CGGAGTGTCTCGTGCCATG	CTGCTCGGCTCTTCTTGGCCATGGAGAAGGGCAGGCATA	966	
Db	1589	CGGAGTGTCTCGTGCCATG	CTGCTCGGCTCTTCTTGGCCATGGAGAAGGGCAGGCATA	1648	
Qy	967	TGGAGTATGAATGCCCCCTA	CTTGGTATATGTGCGCCGTGTGCTCGCTTTCGGCTTGGAGCCCA	1026	
Db	1649	TGGAGTATGAATGCCCCCTA	CTTGGTATATGTGCGCCGTGTGCTCGCTTTCGGCTTGGAGCCCA	1708	
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Db	1709	AGGATGGGAAGGTATGTTT	GCAGTCGATGGGGAATTGATGTTAGCAGAGCCGTGACGG	1769	
Qy	1087	GCCAGGTGCACCAACTACT	CTTCGTGATGGTCAAGCGGTTGCGTGGAGGCCGCCGCCAGCT	1146	
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RESULT 3

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US-10-354-358-25
; Sequence 25, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Pong-ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 69863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1442, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,

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Db 813 TCGTGTCTCTGCACACGGCTTTCGGGGCTCGGCTCTTCTCTGTGTCTAGCCCTGGGCTGGG 872
QY 547 GCTTCATTCTGATGTGGACCTAGAGAGTGAGAAGTATCGGGCTCTGGGGGAGATGCGCT 606
Db 873 GCTTCATTCTGATGTGGACCTAGAGAGTGAGAAGTATCGGGCTCTGGGGGAGATGCGCT 932
QY 607 TCACTCTGGGCACTTCTCTGGCTCTGGGAGCTTGGGCACTTACCGCGGCGCACTGGCTT 666
Db 933 TCACTCTGGGCACTTCTCTGGCTCTGGGAGCTTGGGCACTTACCGCGGCGCACTGGCT 992
QY 667 ACTCTCCCTCTAGAGAGTGGGTTCACAGACACCTGCTCCCGCTGGTGGTCCAGCAGG 726
Db 993 ACTCTCCCTCTAGAGAGTGGGTTCAGAGACACCTGCTCCCGCTGGTGGTCCAGCAGG 1052
QY 727 GCCCGGTAGATGCACACCTTGTGCCACTGGAGAGCCAGTGCCTCTCTCACTGGACAGTGG 786
Db 1053 GCCCGGTAGATGCACACCTTGTGCCACTGGAGAGCCAGTGCCTCTCTCACTGGACAGTGG 1112
QY 787 TGCCTGAGAGACATTTGTGCTAGTCTCTGGGCACTGCTGCACCTGGGCACTGAGA 846
Db 1113 TGCCTGAGAGACATTTGTGCTAGTCTCTGGGCACTGCTGCACCTGGGCACTGAGA 1172
QY 847 TGTCTGTCTGCACACCTTGGGCGCTGTGCAGCTGGGCTCATGCTCTGTCTACGTGCGGG 906
Db 1173 TGTCTGTCTGCACACCTTGGGCGCTGTGCAGCTGGGCTCATGCTCTGTCTACGTGCGGG 1232
QY 907 CGGGAGTGTCTGCTGCCATGTCTGCTGCGCTCTTCTGCGCCATGGAGAGCGAGGCATA 966
Db 1233 CGGGAGTGTCTGCTGCCATGTCTGCTGCGCTCTTCTGCGCCATGGAGAGCGAGGCATA 1292
QY 967 TGGAGTATGAATGCCCTACTTGGTATATGTGCCGCTGGTGGCTTGGAGGCCA 1026
Db 1293 TGGAGTATGAATGCCCTACTTGGTATATGTGCCGCTGGTGGCTTGGAGGCCA 1352
QY 1027 AGGATGGAGAGGTATGTTTGCAGTGGATGGGGAATTGATGTTAGCGAGGCGGTCAGG 1086
Db 1353 AGGATGGAGAGGTATGTTTGCAGTGGATGGGGAATTGATGTTAGCGAGGCGGTCAGG 1412
QY 1087 GCCAGTGCACCCAACTACTTCTGGATGGTTCAGCGGTTGGGAGCCCGGCCAGCT 1146
Db 1413 GCCAGTGCACCCAACTACTTCTGGATGGTTCAGCGGTTGGGAGCCCGGCCAGCT 1472
QY 1147 GGAAGCCCCAGAGATGCCACCGCCAGAGAGCCCTTATGTC 1189
Db 1473 GGAAGCCCCAGAGATGCCACCGCCAGAGAGCCCTTATGACC 1515

RESULT 4
US-10-723-860-721
; Sequence 721, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 721
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-721

Query Match 96.5%; Score 1162.6; DB 20; Length 1783;
Best Local Similarity 98.4%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGCACGAGAGCCCGGGTTCAGAGTTATGATCCAGGGGCGGGCCCCCGGGCGGTGCTCC 66
Db 311 GGCACGAGAGCCCGGGTTCAGAGTTATGATCCAGGGGCGGGCCCCCGGGCGGTGCTCC 370
QY 67 CGGGCCCCCTGCGCGTGTCTGTCTGCTGAAACCCCGCGGGCGGGCAAGGGCAAGGCTTGC 126
Db 371 CGGGCCCCCTGCGCGTGTCTGTCTGCTGAAACCCCGCGGGCGGGCAAGGGCAAGGCTTGC 430
QY 127 AGCTCTTCCGAGTACAGTCGAGCCCTTTTGGCTGAGGCTGAAATCTCTTCACGCTGA 186
Db 431 AGCTCTTCCGAGTACAGTCGAGCCCTTTTGGCTGAGGCTGAAATCTCTTCACGCTGA 490
QY 187 TGCTCACTAGCGCGGGAACCAACGCGGGGAGCTGTGTGCGGTGCGAGAGCTGGGCGCT 246
Db 491 TGCTCACTAGCGCGGGAACCAACGCGGGGAGCTGTGTGCGGTGCGAGAGCTGGGCGCT 550
QY 247 GGGAGCGCTTGGTGTCTGTGAGACCGGCTGATGTCACAGAGTGTGTAAACGGGCTCA 306
Db 551 GGGAGCGCTTGGTGTCTGTGAGACCGGCTGATGTCACAGAGTGTGTAAACGGGCTCA 610
QY 307 TGGAGCGGCTTGAATGGGAGACCGCATCCAGAAAGCCCTGTGTAGCCTCCACAGCAGCT 366
Db 611 TGGAGCGGCTTGAATGGGAGACCGCATCCAGAAAGCCCTGTGTAGCCTCCACAGCAGCT 670
QY 367 CTGGCAACGCGCTGGCAGCTTCTTGAACCAATATGTGTGCTATGAGCAGGTCAACCAATG 426
Db 671 CTGGCAACGCGCTGGCAGCTTCTTGAACCAATATGTGTGCTATGAGCAGGTCAACCAATG 730
QY 427 AAGACCTCTGACCACTGCGAGCTTATGCTGTGCGCGCGGCTGTGTACCCATGACAC 486
Db 731 AAGACCTCTGACCACTGCGAGCTTATGCTGTGCGCGCGGCTGTGTACCCATGACAC 790
QY 487 TGCTGTCTCTGACACGCGCTTGGGGCTGCGCTCTTCTGTGTCTGACGCTGGCCTGGG 546
Db 791 TGCTGTCTCTGACACGCGCTTGGGGCTGCGCTCTTCTGTGTCTGACGCTGGCCTGGG 850
QY 547 GCTTCAATGTGTGTGTGACCTAGAGAGTGAAGAATTCGGCGTCTGGGGGAGATGCGCT 606
Db 851 GCTTCAATGTGTGTGTGACCTAGAGAGTGAAGAATTCGGCGTCTGGGGGAGATGCGCT 910
QY 607 TCACCTGCGGCACTTCTGCGTCTGCGAGCTTGGCAGCTTACCGGGCGGCTTGGGCTT 666
Db 911 TCACCTGCGGCACTTCTGCGTCTGCGAGCTTGGCAGCTTACCGGGCGGCTTGGGCTT 970
QY 667 ACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGGCTGTGTGCTCCAGCAGG 726
Db 971 ACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGGCTGTGTGCTCCAGCAGG 1030
QY 727 GCCCGGTAGATGCACACCTTGTGCACTGGAGAGCCAGTGCCTCTCTCACTGGACAGTGG 786
Db 1031 GCCCGGTAGATGCACACCTTGTGCACTGGAGAGCCAGTGCCTCTCTCACTGGACAGTGG 1090
QY 787 TGCCCGGAGGAGCTTGTGTGTAGTCTGCGACCTGCGCTGCACTCGACCTGGGCACTGAGA 846
Db 1091 TGCCCGGAGGAGCTTGTGTGTAACTCTGCGACCTGCTGCACTCGACCTGGGCACTGAGA 1150
QY 847 TGTCTGTCTGACCCCATGGGCGCTGTGAGCTGGGCTCATGCACTCTGTCTTACCTGGCGGG 906
Db 1151 TGTCTGTCTGACCCCATGGGCGCTGTGAGCTGGGCTCATGCACTCTGTCTTACCTGGCGGG 1210
QY 907 CGGAGTGTCTGTCGCAATGCTGCGCTCTTCTGCGCCATGGAGAGCGGCAATGATA 966
Db 1211 CGGAGTGTCTGTCGTCATGCTGCTGCGCTTCTTCTGGCCATGGAGAGCGGCAATGATA 1270
QY 967 TGGAGTATGAATGCCCTACTTGTGTATATGTGCCGCTGCTGCGCTTCCGCTTGGAGGCCA 1026
Db 1271 TGGAGTATGAATGCCCTACTTGTGTATATGTGCCGCTGCTGCGCTTCCGCTTGGAGGCCA 1330
QY 1027 AGGATGGAGAGGTATGTTTGCAGTGGATGGGGAATTTGATGTTAGCGAGGCGGCTGACGG 1086
Db 1331 AGGATGGAGAGGTATGTTTGCAGTGGATGGGGAATTTGATGTTAGCGAGGCGGCTGACGG 1390

		NAME/KEY: SITE		95.4%; Score 1149.4; DB 10; Length 1533;			
		LOCATION: (1527)		Best Local Similarity 98.3%; Pred. No. 2.2e-312;			
		OTHER INFORMATION: n equals a,t,g, or c		Matches 1164; Conservative 6; Mismatches 13; Indels 1; Gaps 1;			
		US-09-933-767-90					
		Query Match					
QY	7	GGCAGAGAGCGCGGGTCGAGGTATATGATCCAGCGGGCGGCCCGCGGGCGTGTCTCC	66				
Db	47	GGCAGCGGAGCGCGGGTCGAGGTATATGATCCAGCGGGCGGCCCGCGGGCGTGTCTCC	106				
QY	67	CGCGCCCTGCCCGCTGCTGCTGAACCCCGCGGGCGGCAAGGCAAGGCTTGC	126				
Db	107	CGCGCCCTGCCCGGTGCTGCTGAACCCCGCGGGCGGCAAGGCAAGGCTTGC	166				
QY	127	AGCTCTCCCGAGTCACGTCGAGTCCAGTCCAGCGGGCGGCCCGCGGGCGTGTCTCC	186				
Db	167	AGCTCTCCCGAGTCACGTCGAGTCCAGTCCAGCGGGCGGCCCGCGGGCGTGTCTCC	226				
QY	187	TGCTCACTGACCGCGGNAACACCGCGGGAGCTGTGTCGTCGAGAGCTGGGCGCT	246				
Db	227	TGCTCACTGACCGCGGNAACACCGCGGGAGCTGTGTCGTCGAGAGCTGGGCGCT	286				
QY	247	GGGACGCTCTGTCGTGATGTCGAGAGCGGCTGATGTCACGAGTGTGTAACGGGC	305				
		RESULT 6					
		US-10-004-860-90					
		Sequence 90, Application US/10004860					
		Publication No. US20030065160A1					
		GENERAL INFORMATION:					
		APPLICANT: Young et al.					
		TITLE OF INVENTION: 207 Human Secreted Proteins					
		FILE REFERENCE: P2007P1					
		CURRENT APPLICATION NUMBER: US/10/004,860					
		CURRENT FILING DATE: 2001-12-07					
		Prior Application removed - See File Wrapper or Palm					
		NUMBER OF SEQ ID NOS: 1227					
		SOFTWARE: PatentIn Ver. 2.0					
		SEQ ID NO 90					
		LENGTH: 1533					
		TYPE: DNA					
		ORGANISM: Homo sapiens					
		FEATURE:					
		NAME/KEY: SITE					
		LOCATION: (12)					
		OTHER INFORMATION: n equals a,t,g, or c					
		FEATURE:					
		NAME/KEY: SITE					
		LOCATION: (1522)					
		OTHER INFORMATION: n equals a,t,g, or c					
		FEATURE:					
		NAME/KEY: SITE					
		LOCATION: (1527)					
		OTHER INFORMATION: n equals a,t,g, or c					
		US-10-004-860-90					
		Query Match		95.4%; Score 1149.4; DB 14; Length 1533;			
		Best Local Similarity		98.3%; Pred. No. 2.2e-312;			
		Matches 1164; Conservative		6; Mismatches 13; Indels 1; Gaps 1;			
QY	7	GGCAGAGAGCGCGGGTCGAGGTATATGATCCAGCGGGCGGCCCGCGGGCGTGTCTCC	66				
Db	47	GGCAGCGGAGCGCGGGTCGAGGTATATGATCCAGCGGGCGGCCCGCGGGCGTGTCTCC	106				
QY	67	CGCGCCCTGCCCGCTGCTGCTGAACCCCGCGGGCGGCAAGGCAAGGCTTGC	126				
Db	107	CGCGCCCTGCCCGGTGCTGCTGAACCCCGCGGGCGGCAAGGCAAGGCTTGC	166				
QY	127	AGCTCTCCCGAGTCACGTCGAGTCCAGTCCAGCGGGCGGCCCGCGGGCGTGTCTCC	186				
Db	167	AGCTCTCCCGAGTCACGTCGAGTCCAGTCCAGCGGGCGGCCCGCGGGCGTGTCTCC	226				
QY	187	TGCTCACTGACCGCGGNAACACCGCGGGAGCTGTGTCGTCGAGAGCTGGGCGCT	246				
Db	227	TGCTCACTGACCGCGGNAACACCGCGGGAGCTGTGTCGTCGAGAGCTGGGCGCT	286				
QY	247	GGGACGCTCTGTCGTGATGTCGAGAGCGGCTGATGTCACGAGTGTGTAACGGGC	305				

Db	287	GBRAGCCTCTGGTGTGATGTTGGAGCGGCTGATGCACGAGTGGTGAACGGCTTC	346	;	CURRENT FILING DATE: 2001-12-20
Qy	306	ATGGAGCGGCTGACTGGGAGACCGGCATTCAGAGCGCCCTGTGTAGCTCCAGCAGGC	365	;	EARLIER FILING DATE: 1998-12-04
Db	347	ATGGAGCGGCTGACTGGGAGACCGGCATTCAGAGCGCCCTGTGTAGCTCCAGCAGGC	406	;	EARLIER FILING DATE: 1998-06-04
Qy	366	TCGTGCAACGCGCTGGCAGCTTCCTTGACCAATATGCTGGCTATGAGCAGGTCAACCAAT	425	;	EARLIER FILING DATE: 1997-06-06
Db	407	TCGTGCAACGCGCTGGCAGCTTCCTTGACCAATATGCTGGCTATGAGCAGGTCAACCAAT	466	;	EARLIER FILING DATE: 1997-06-06
Qy	426	GAAGACCTCTGACCAACTGACGCTATTGCTGCGCGGCTGCTGTCAACCAATGAAC	485	;	EARLIER FILING DATE: 1997-06-06
Db	467	GAAGACCTCTGACCAACTGACGCTATTGCTGCGCGGCTGCTGTCAACCAATGAAC	526	;	EARLIER FILING DATE: 1997-06-06
Qy	486	CTGCTGTCTGTGACACGCGCTTCGGGGCTGGCGCTTCTCTGTGTGCTAGCCCTGGCCTGG	545	;	EARLIER FILING DATE: 1997-06-06
Db	527	CTGCTGTCTGTGACACGCGCTTCGGGGCTGGCGCTTCTCTGTGTGCTAGCCCTGGCCTGG	586	;	EARLIER FILING DATE: 1997-06-06
Qy	546	GGCTTCATTCCTGATGTGACCTAGAGAGTGAAGTATCGGCGTCTGGGGGAGATGCGC	605	;	EARLIER FILING DATE: 1997-06-06
Db	587	GGCTTCATTCCTGATGTGACCTAGAGAGTGAAGTATCGGCGTCTGGGGGAGATGCGC	646	;	EARLIER FILING DATE: 1997-06-06
Qy	606	TTCACTCTCGGCACTTCTCTGGCTCTGGCAGCCTTTCGCGCACTTACCGCGCCGCACTGGCT	665	;	EARLIER FILING DATE: 1997-06-06
Db	647	TTCACTCTCGGCACTTCTCTGGCTCTGGCAGCCTTTCGCGCACTTACCGCGCCGCACTGGCC	706	;	EARLIER FILING DATE: 1997-06-06
Qy	666	TACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGCTTGTGTGTCAGCAG	725	;	EARLIER FILING DATE: 1997-06-06
Db	707	TACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGCTTGTGTGTCAGCAG	766	;	EARLIER FILING DATE: 1997-06-06
Qy	726	GGCCCGGTAGATGACACCTTGTGCTAGTGTGCTGAGGAGCGAGTGCCTCTCACTGGACAGTG	785	;	EARLIER FILING DATE: 1997-06-06
Db	767	GGCCCGGTAGATGACACCTTGTGCTAGTGTGCTGAGGAGCGAGTGCCTCTCACTGGACAGTG	826	;	EARLIER FILING DATE: 1997-06-06
Qy	786	GTCCCGGACGAGACTTGTGCTAGTGTGCTGAGTGTGCTGAGGAGCGAGTGCCTCTCACTGGACAGTG	845	;	EARLIER FILING DATE: 1997-06-06
Db	827	GTCCCGGACGAGACTTGTGCTAGTGTGCTGAGTGTGCTGAGGAGCGAGTGCCTCTCACTGGACAGTG	886	;	EARLIER FILING DATE: 1997-06-06
Qy	846	ATGTTTGTCTGACCCATGGGCGCTGTGCAAGTGGGCTGATGCTGCTTACGTGCGG	905	;	EARLIER FILING DATE: 1997-06-06
Db	887	ATGTTTGTCTGACCCATGGGCGCTGTGCAAGTGGGCTGATGCTGCTTACGTGCGG	946	;	EARLIER FILING DATE: 1997-06-06
Qy	906	CGGGAGTGTCTGTCGCACTGCTGCGGCTTCTTCTGCGCATGAGAGGCGAGGCAGGCAT	965	;	EARLIER FILING DATE: 1997-06-06
Db	947	CGGGAGTGTCTGTCGCACTGCTGCGGCTTCTTCTGCGCATGAGAGGCGAGGCAGGCAT	1006	;	EARLIER FILING DATE: 1997-06-06
Qy	966	ATGGAGTATCAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCCGCTTGGAGGCC	1025	;	EARLIER FILING DATE: 1997-06-06
Db	1007	ATGGAGTATCAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCCGCTTGGAGGCC	1066	;	EARLIER FILING DATE: 1997-06-06
Qy	1026	AAGGATGGGAAGGTATGTTGCAATGGGAAATGATGTTAGCGAGCGCGTGCAG	1085	;	EARLIER FILING DATE: 1997-06-06
Db	1067	AAGGATGGGAAGGTATGTTGCAATGGGAAATGATGTTAGCGAGCGCGTGCAG	1126	;	EARLIER FILING DATE: 1997-06-06
Qy	1086	GGCCAGGTGACCAACACTTCTGATGGTTCAGCGGTTGCGTGGAGCCCGCCCGCAGC	1145	;	EARLIER FILING DATE: 1997-06-06
Db	1127	GGCCAGGTGACCAACACTTCTGATGGTTCAGCGGTTGCGTGGAGCCCGCCCGCAGC	1186	;	EARLIER FILING DATE: 1997-06-06
Qy	1146	TGGAAGCCCCGACGAGTGCACCGCCAGAGAGCCCTTATGATC	1189	;	EARLIER FILING DATE: 1997-06-06
Db	1187	TGGAAGCCCCGACGAGTGCACCGCCAGAGAGCCCTTATGACC	1230	;	EARLIER FILING DATE: 1997-06-06

RESULT 7
US-10-023-282-90
; Sequence 90, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282

; EARLIER APPLICATION NUMBER: 60/048, 877
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 878
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/070, 923
 ; EARLIER FILING DATE: 1997-12-18
 ; EARLIER APPLICATION NUMBER: 60/092, 921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/094, 657
 ; EARLIER FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1227
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 90
 ; LENGTH: 1533
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (12)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (123)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1522)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1527)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-10-023-282-90

Query Match 95.4%; Score 1149.4; DB 14; Length 1533;
 Best Local Similarity 98.3%; Pred. No. 2.2e-312;
 Matches 1164; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY	7	GGCAGAGAGCGCGGTGCGAGTTATGGATCCAGCGGGGGCGCCCGGGGGCGTGTCC	66
Db	47	GGCAGCGGAGCGCGGGTTCAGAGTTATGGATCCAGCGGGGGCGCCCGGGGGCGTGTCC	106
QY	67	CGCGCCCTGCGCGTGTGTGCTGAACCCGCGCGGGCAAGGCGGCTTGC	126
Db	107	CGCGCCCTGCGCGTGTGTGCTGAACCCGCGCGGGCAAGGCGGCTTGC	166
QY	127	AGCTCTCCGGAGTCACGTGCAGCGCCCTTTTGGCTGAGGCTGAATCTCTTCAGCGCTGA	186
Db	167	AGCTCTCCGGAGTCACGTGCAGCGCCCTTTTGGCTGAGGCTGAATCTCTTCAGCGCTGA	226
QY	187	TGCTCACTGAGCGCGGAACACCGCGCGGAGCTGTGTGGTTCGGAGGAGCTGGGCGGCT	246
Db	227	TGCTCACTGAGCGCGGAACACCGCGCGGAGCTGTGTGGTTCGGAGGAGCTGGGCGGCT	286
QY	247	GGGAGCGCTGTGTGTCTATGCTGAGACGGGCTCATGACAGAGTGTGAACGGGC-TC	305
Db	287	GGGAGCGCTGTGTGTCTATGCTGAGACGGGCTCATGACAGAGTGTGAACGGGCTTC	346
QY	306	ATGGAGCGGCTGACTGGGAGACCGCCATCCAGAAAGCCCTGTGTGAGCTCCAGCAGGC	365
Db	347	ATGGAGCGGCTGACTGGGAGACCGCCATCCAGAAAGCCCTGTGTGAGCTCCAGCAGGC	406
QY	366	TCTGCAACCGCTGGAGCTTCCTTGAACCTATGCTGGTATGAGCAGGTCAACCAAT	425
Db	407	TCTGCAACCGCTGGAGCTTCCTTGAACCTATGCTGGTATGAGCAGGTCAACCAAT	466
QY	426	GAAGACCTCTTGACCAACTGTCAGCGCTATGCTGCGCGGCTGCTGTCAACCAATGAAC	485
Db	467	GAAGACCTCTTGACCAACTGTCAGCGCTATGCTGCGCGGCTGCTGTCAACCAATGAAC	526
QY	486	CTGCTGTCTTGACACAGGCTTCGGGGTGGCGCTCTTCTGTGCTCAGCTGGCGCTGG	545
Db	527	CTGCTGTCTTGACACAGGCTTCGGGGTGGCGCTCTTCTGTGCTCAGCTGGCGCTGG	586

QY	546	GGCTTCATTGCTGATGTGGACCTAGAGTGAGAGTATCGGCGCTTGGGGGAGATGGCC	605
Db	587	GGCTTCATTGCTGATGTGGACCTAGAGTGAGAGTATCGGCGCTTGGGGGAGATGGCC	646
QY	606	TTCACTCTGGGCACTTTCTGCGCTTGGCAGCTTGGCACTTACCGCGGCGGACTGGCT	665
Db	647	TTCACTCTGGGCACTTTCTGCGCTTGGCAGCTTGGCACTTACCGCGGCGGACTGGCC	706
QY	666	TACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCTCCCGGTGTGGTCCAGCAG	725
Db	707	TACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCTCCCGGTGTGGTCCAGCAG	766
QY	726	GGCCCGGTAGATGCACACCTTGTGCCACTGGAGAGCAGTGCCTCTCACTGACACAGTG	785
Db	767	GGCCCGGTAGATGCACACCTTGTGCCACTGGAGAGCAGTGCCTCTCACTGACACAGTG	826
QY	786	GTGCCCGACGAGGACTTTGTGTAGTCTTGGCACTGTGCACTCGCACTGGGCACTGAG	845
Db	827	GTGCCCGACGAGGACTTTGTGTAGTCTTGGCACTGTGCACTCGCACTGGGCACTGAG	886
QY	846	ATGTTTGTGCACCCATGGGCGCTGTGCAGCTGGCGTCACTGCACTGTCTTACGTGGG	905
Db	887	ATGTTTGTGCACCCATGGGCGCTGTGCAGCTGGCGTCACTGCACTGTCTTACGTGGG	946
QY	906	CGCGGAGTGTCTGTCGCACTGCTGGGCTCTTCTGGCCATGGAGAGGCGGAGCAT	965
Db	947	CGCGGAGTGTCTGTCGCACTGCTGGGCTCTTCTGGCCATGGAGAGGCGGAGCAT	1006
QY	966	ATGGAGTATGAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCCGCTTGGAGGCC	1025
Db	1007	ATGGAGTATGAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCCGCTTGGAGGCC	1066
QY	1026	AAGATCGGAAAGGTATGTTTGCAGTGGATGGGAAATGATGTTAGCGAGGCGGTGCAG	1085
Db	1067	AAGATCGGAAAGGTATGTTTGCAGTGGATGGGAAATGATGTTAGCGAGGCGGTGCAG	1126
QY	1086	GGCCAGGTGCACCCCAACTACTTCTGGATGCTGACGCGTTCGCTGGAGCGCCCGCCAGC	1145
Db	1127	GGCCAGGTGCACCCCAACTACTTCTGGATGCTGACGCGTTCGCTGGAGCGCCCGCCAGC	1186
QY	1146	TGGAAGCCCGCAGCAGATGCCACCCAGAGAGCCCTTATGATC	1189
Db	1187	TGGAAGCCCGCAGCAGATGCCACCCAGAGAGCCCTTATGATC	1230

RESULT 8

US-09-970-516-1
 ; Sequence 1, Application US/09970516
 ; Patent No. US20020099029A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20020099029A1artis AG
 ; TITLE OF INVENTION: Induction of blood vessel formation through administration of
 ; FILE REFERENCE: 4-31617
 ; CURRENT APPLICATION NUMBER: US/09/970,516
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1155)
 ; OTHER INFORMATION:
 ; US-09-970-516-1

Query Match 95.2%; Score 1147; DB 9; Length 1155;
 Best Local Similarity 99.6%; Pred. No. 1e-311;
 Matches 1150; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 33 ATGGATCCAGCGCGGCCCCCGGGCGTGTCTCCCGCGCCCTCGCGCGTGTGGTGTCTG 92
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 ATGGATCCAGCGCGGCCCCCGGGCGTGTCTCCCGCGCCCTCGCGCGTGTGGTGTCTG 60
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
93 CTGAACCCCGCGCGGCGCAAGGCGCTTTCAGAGCTTTCGGAGTCACTGTCAGGCC 152
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CTGAACCCCGCGCGGCGCAAGGCGCTTTCAGAGCTTTCGGAGTCACTGTCAGGCC 120
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
153 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGGAACACCGG 212
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGGAACACCGG 180
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
213 CGGGAGCTGTGGTGTGGAGAGCTTGGCGCTGGAGAGCTCTGGTGTCTATGCTGA 272
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 CGGGAGCTGTGGTGTGGAGAGCTTGGCGCTGGAGAGCTCTGGTGTCTATGCTGA 240
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
273 GACGGCTGATGACGAGGTGTGAAACGGGCTCATGGAGCGGCTGAATGGAGACCGCC 332
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GACGGCTGATGACGAGGTGTGAAACGGGCTCATGGAGCGGCTGAATGGAGACCGCC 300
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
333 ATCCAGAACCCCTGTGTAGCTTCCAGCAGAGCTCTGGCAACCGCTGACGCTTCTTG 392
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 ATCCAGAACCCCTGTGTAGCTTCCAGCAGAGCTCTGGCAACCGCTGACGCTTCTTG 360
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
393 AACCATTTATGCTGCTATGAGCAGGTCAACATGAAGACTCTCTGACCAACTGACGCTA 452
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AACCATTTATGCTGCTATGAGCAGGTCAACATGAAGACTCTCTGACCAACTGACGCTA 420
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
453 TTGCTGTGCGCGGCTGTCTCACCCTATGAACCTGTCTCTCTGCACACGGCTTCGGG 512
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TTGCTGTGCGCGGCTGTCTCACCCTATGAACCTGTCTCTCTGCACACGGCTTCGGG 480
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
513 CTGCGCTCTTCTCTGTGTCTGCTGAGCTGCGGCTTCAATGCTGATGTGACCTAGAG 572
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 CTGCGCTCTTCTCTGTGTCTGCTGAGCTGCGGCTTCAATGCTGATGTGACCTAGAG 540
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
573 AGTGAGAGTATCGGCTGTGGGGGAGATGCGCTTCACTCTGGGCACTTCTCGCTCTG 632
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGTGAGAGTATCGGCTGTGGGGGAGATGCGCTTCACTCTGGGCACTTCTCGCTCTG 600
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
633 GCAGCTTGGGCACTTACCGCGCGGCACTGGCTTACCTCCCTTAGGAAGAGTGGGTTC 692
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GCAGCTTGGGCACTTACCGCGCGGCACTGGCTTACCTCCCTTAGGAAGAGTGGGTTC 660
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
693 AAGACACTCTCTCCCGTGTGTGTCTCAGCAGGCGCGGTAGATGACACCTTGTGCCA 752
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 AAGACACTCTCTCCCGTGTGTGTCTCAGCAGGCGCGGTAGATGACACCTTGTGCCA 720
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
753 CTGGAGAGCCAGTGCCTCTCACTGGAACAGTGTGGTGGCCGACGAGGACTTGTGTAGTC 812
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 CTGGAGAGCCAGTGCCTCTCACTGGAACAGTGTGGTGGCCGACGAGGACTTGTGTAGTC 780
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813 CTGGCACTGTGCACTCGCACTTGGGCACTGAGATGTTGTCTGCACCATGGGCGGCTGT 872
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781 CTGGCACTGTGCACTCGCACTTGGGCACTGAGATGTTGTCTGCACCATGGGCGGCTGT 840
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
873 GCAGCTGGCTCACTGCACTGTCTACGTGCGGCGGGAGTGTCTGTGCACTGTGCTG 932
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841 GCAGCTGGCTCACTGCACTGTCTACGTGCGGCGGGAGTGTCTGTGCACTGTGCTG 900
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
933 CGCTCTTCTTGGCCATGAGAGAGGCAATGAGATGATGATGATGATGATGATGATGAT 992
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901 CGCTCTTCTTGGCCATGAGAGAGGCAATGAGATGATGATGATGATGATGATGATGAT 960
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
993 TATGTGCGCTGTGTGCTTCCGCTTGGAGCGGCAAGGATGGAAGGATGTTTGTGAGTG 1052
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 TATGTGCGCTGTGTGCTTCCGCTTGGAGCGGCAAGGATGGAAGGATGTTTGTGAGTG 1020
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1053 GATGGGAATTTGATGTTTGTGAGGCGGCTGTGAGGCGGCAAGGATGATGATGATGATGAT 1112
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 GATGGGAATTTGATGTTTGTGAGGCGGCTGTGAGGCGGCAAGGATGATGATGATGATGAT 1080
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1113 ATGTGTCAGCGGTGTGCTGAGGCCCCCGCCAGCTGTGGAAGCCCCAGCAGATGCCACCGCCA 1172

Db 1081 ATGCTCAGCGTGTGGTGGAGCCCCCGCCAGCTTGAAGCCCCAGATGCCACGCCA 1140
QY 1173 GAAGAGCCCTTATGA 1187
Db 1141 GAAGAGCCCTTATGA 1155
RESULT 9
US-10-619-344-1
; Sequence 1, Application US/10619344
; Publication No. US20040086487A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/10/619,344
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/970,516
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-10-619-344-1

Query Match 95.2%; Score 1147; DB 18; Length 1155;
Best Local Similarity 99.6%; Pred. No. 1e-311; 5; Indels 0; Gaps 0;
Matches 1150; Conservative 0; Mismatches 5

QY 33 ATGGATCCAGCGGCGGCCCCCGGGCGTGTCTCCCGCGCCCTCGCGCGTGTGGTGTCTG 92
Db 1 ATGGATCCAGCGGCGGCCCCCGGGCGTGTCTCCCGCGCCCTCGCGCGTGTGGTGTCTG 60
QY 93 CTGAACCCCGCGCGGCGCAAGGCGCTTTCAGAGCTTTCGGAGTCACTGTCAGGCC 152
Db 61 CTGAACCCCGCGCGGCGCAAGGCGCTTTCAGAGCTTTCGGAGTCACTGTCAGGCC 120
QY 153 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGGAACACCGG 212
Db 121 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGGAACACCGG 180
QY 213 CGGGAGCTGTGGTGTGGAGAGCTTGGCGCTGGGAGCGCTCTGGTGTCTATGCTTGA 272
Db 181 CGGGAGCTGTGGTGTGGAGAGCTTGGCGCTGGGAGCGCTCTGGTGTCTATGCTTGA 240
QY 273 GACGGCTGATGACGAGGTGTGAAACGGGCTCATGGAGCGGCTGAATGGAGACCGCC 332
Db 241 GACGGCTGATGACGAGGTGTGAAACGGGCTCATGGAGCGGCTGAATGGAGACCGCC 300
QY 333 ATCCAGAACCCCTGTGTAGCTTCCAGCAGAGCTCTGGCAACCGCTGACGCTTCTTG 392
Db 301 ATCCAGAACCCCTGTGTAGCTTCCAGCAGAGCTCTGGCAACCGCTGACGCTTCTTG 360
QY 393 AACCATTTATGCTGCTATGAGCAGGTCAACATGAAGACTCTCTGACCAACTGACGCTA 452
Db 361 AACCATTTATGCTGCTATGAGCAGGTCAACATGAAGACTCTCTGACCAACTGACGCTA 420
QY 453 TTGCTGTGCGCGGCTGTCTCACCCTATGAACCTGTCTCTCTGCACACGGCTTCGGG 512
Db 421 TTGCTGTGCGCGGCTGTCTCACCCTATGAACCTGTCTCTCTGCACACGGCTTCGGG 480
QY 513 CTGCGCTCTTCTCTGTGTCTGCTGAGCTGCGGCTTCAATGCTGATGTGACCTAGAG 572
Db 481 CTGCGCTCTTCTCTGTGTCTGCTGAGCTGCGGCTTCAATGCTGATGTGACCTAGAG 540

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OM protein - protein search, using sw model

Run on: June 15, 2005, 11:44:06 ; Search time 174 Seconds
(without alignments)
1130.106 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 2017
Sequence: 1 MDPAGRGVLPKRCVRLV.....CVEPPPSWKPOQMPPEPL 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	99.8	384	1 SPH1 HUMAN	Q9nyal homo sapien
2	2013	99.8	470	2 Q8N632	Q8n632 homo sapien
3	2006	99.5	384	2 Q96HV8	Q96hv8 homo sapien
4	1996	99.0	398	2 Q96GK1	Q96gk1 homo sapien
5	1644	81.5	329	2 Q9NOA5	Q9noa5 macaca fasc
6	1636.5	81.1	382	2 Q8C115	Q8c115 mus musculus
7	1627.5	80.7	381	2 Q91ZN3	Q91zn3 mus musculus
8	1627.5	80.7	388	2 Q88886	Q88886 mus musculus
9	1624.5	80.5	504	2 Q88885	Q88885 mus musculus
10	1599.5	79.3	383	2 Q642F6	Q642f6 rattus norv
11	1596.5	79.2	383	2 Q91V26	Q91v26 rattus norv
12	1505	74.6	287	2 Q9BTG7	Q9btg7 homo sapien
13	893	44.3	617	1 SPH2 MOUSE	Q9jia7 mus musculus
14	886.5	44.0	616	2 Q6AYB2	Q6ayb2 rattus norv
15	883.5	43.8	654	1 SPH2 HUMAN	Q9nra0 homo sapien
16	579.5	28.7	685	2 Q7QIP4	Q7qip4 anopheles g
17	560	27.8	641	2 Q9VYV8	Q9vyv8 drosophila
18	519	25.7	661	2 Q9V2W0	Q9v2w0 drosophila
19	479.5	23.8	485	2 Q8L7L1	Q8l7l1 arabidopsis
20	449	22.3	1240	2 Q65419	Q65419 arabidopsis
21	409	20.3	624	2 Q86KF9	Q86kf9 dictyosteli
22	378.5	18.8	760	2 Q6B516	Q6b516 dictyosteli
23	375.5	18.6	423	2 Q7JW91	Q7jw91 caenorhabdi
24	375.5	18.6	473	2 Q18425	Q18425 caenorhabdi
25	375	18.6	480	2 Q8H350	Q8h350 oryza sativ
26	357.5	17.7	687	2 Q06147	Q06147 saccharomyc
27	355	17.6	458	2 Q14159	Q14159 schizosacch
28	348	17.3	556	2 Q7S9Y1	Q7s9y1 neurospora
29	346	17.2	624	2 Q12246	Q12246 saccharomyc
30	335	16.6	560	2 Q6FLC1	Q6flc1 candida gla
31	331	16.4	794	2 Q6FMR1	Q6fmr1 candida gla

RESULT 1

SPH1_HUMAN
ID SPH1_HUMAN STANDARD; PRT; 384 AA.
AC Q9NYAL; Q9HD92; Q9NY70; Q9NYL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sphingosine kinase 1 (EC 2.7.1.-) (SK 1) (SPK 1).
GN Name=SPHK1; Synonyms=SPHK, SPK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20323213; PubMed=10863092; DOI=10.1016/S0378-1119(00)00205-5;
RA Melendez A.J., Carloe-Dias E., Gosink M., Allen J.M., Takacs L.;
RT "Human sphingosine kinase: molecular cloning, functional
characterization and tissue distribution.";
RL Gene 251:19-26(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=20263733; PubMed=10802064; DOI=10.1016/S0014-5793(00)01510-6;
RA Nava V.E., Lacana' E., Poulton S., Liu H., Sugiura M., Kono K.,
RA Milsten S., Kohama T., Spiegel S.;
RT "Functional characterization of human sphingosine kinase-1.";
RL FEBS Lett. 473:81-84(2000).
RN [3]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=20407120; PubMed=10947957; DOI=10.1042/0264-6021:3500429;
RA Pitson S.M., D'Andrea R.J., Vandenberg B.W.;
RA Gamble J.R., Vadas M.A., Wattenberg B.W.;
RT "Human sphingosine kinase: purification, molecular cloning and
characterization of the native and recombinant enzymes.";
RL Biochem. J. 350:429-441(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX Van Velthoven P.P., Gijbbers S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland, and Ovary;
PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Hosoda M., Hotuta T.,

ALIGNMENTS

RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara K., Takeuchi K., Arita M.,
RA Imose N., Mueshino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kamagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiraio M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).
CC -!- FUNCTION: Catalyzes the phosphorylation of sphingosine to form
CC sphingosine 1-phosphate (SPP), a lipid mediator with both intra-
CC and extracellular functions. Also acts on D-erythro-sphingosine
CC and to a lesser extent sphinganine, but not other lipids, such as
CC D,L-threo-dihydrosphingosine, N,N-dimethylsphingosine,
CC diacylglycerol, ceramide, or phosphatidylinositol.
CC -!- CATALYTIC ACTIVITY: Sphingosine + ATP = sphingosine 1-phosphate +
CC ADP.
CC -!- SUBUNIT: Binds to calmodulin.
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in adult
CC liver, kidney, heart and skeletal muscle.
CC -!- SIMILARITY: Contains 1 DAGKC domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
DR EMBL; AF266756; AAF73470.1; -;
DR EMBL; AF238083; AAF73423.1; -;
DR EMBL; AF200328; AAG01980.1; -;
DR EMBL; AK023393; BAB14558.1; -;
DR EMBL; AK022402; BAB14028.1; -;
DR EMBL; AJ245504; CAB92131.1; -;
DR Gene; HGNC:11240; SPHK1.
DR H-InvDB; HIX0022906; -;
DR MIM; 603730; -;
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005524; F:ATP binding; IDA.
DR GO; GO:0005516; F:calmodulin binding; IDA.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; IDA.
DR GO; GO:0000287; F:magnesium ion binding; IDA.
DR GO; GO:0006916; F:anti-apoptosis; TAS.
DR GO; GO:0019722; P:calcium-mediated signaling; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0045766; P:positive regulation of angiogenesis; IDA.
DR GO; GO:0030307; P:positive regulation of cell growth; IDA.
DR GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR GO; GO:0045931; P:positive regulation of mitotic cell cycle; IDA.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. .; IDA.
DR GO; GO:0046521; P:sphingoid catabolism; NAS.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM000046; DAGKC; 1.
KW ATP-binding; Calmodulin-binding; Kinase; Transferase.
FT CONFLICT 6 6 Missing (in Ref. 4).
FT CONFLICT 11 15 LPRPC -> ARL (in Ref. 4).

FT	CONFLICT	114	115	NA -> KP (in Ref. 4).
FT	CONFLICT	251	251	V -> M (in Ref. 2).
FT	CONFLICT	260	260	V -> I (in Ref. 2).
FT	CONFLICT	302	302	L -> F (in Ref. 2).
FT	CONFLICT	325	325	V -> G (in Ref. 4).
FT	CONFLICT	337	337	V -> M (in Ref. 3).
SQ	SEQUENCE	384 AA;	42517 MW;	EB04A7F2034C2DB0 CRC64;

Query Match 99.8%; Score 2013; DB 1; Length 384;
Best Local Similarity 99.7%; Pred. No. 7.3e-163;
Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDPAGGPRGVLP	PRCRVILVLLNPRGGGKQALQ	LFRRSHVQPLLAFAEISFTLMLTERRNHA	60
Db	1	MDPAGGPRGVLP	PRCRVILVLLNPRGGGKQALQ	LFRRSHVQPLLAFAEISFTLMLTERRNHA	60
Qy	61	RELVRSEELGRWDALV	VMGSDGLMHEVVGMLMERPDWETA	IQKPLCSLPAGSGNALAASL	120
Db	61	RELVRSEELGRWDALV	VMGSDGLMHEVVGMLMERPDWETA	IQKPLCSLPAGSGNALAASL	120
Qy	121	NYAGYEQVTNEDLLT	NCTLLCRLLSPMNLISLHTASGLR	LFSLVSLAWGFIADVDLE	180
Db	121	NYAGYEQVTNEDLLT	NCTLLCRLLSPMNLISLHTASGLR	LFSLVSLAWGFIADVDLE	180
Qy	181	SEKYRRLGEMRFTLT	FLRLAALTYRGLAYLPVGRVSKTPAS	PVVVVOGQGPVDAHLVP	240
Db	181	SEKYRRLGEMRFTLT	FLRLAALTYRGLAYLPVGRVSKTPAS	PVVVVOGQGPVDAHLVP	240
Qy	241	LEEPVPSHWTVPDE	DFVLVLLHSLGSEMFAAPMGRCAAG	VMHLYFYVRAGVSRMLL	300
Db	241	LEEPVPSHWTVPDE	DFVLVLLHSLGSEMFAAPMGRCAAG	VMHLYFYVRAGVSRMLL	300
Qy	301	RLFLAMEKGRHMEY	CEPYLVYPVPAFRLEPKDGMFPA	VDGELMVSEAVQGVHPNYFW	360
Db	301	RLFLAMEKGRHMEY	CEPYLVYPVPAFRLEPKDGMFPA	VDGELMVSEAVQGVHPNYFW	360
Qy	361	MVSGCVPFPPSWK	PQOMPPEEPL	384	
Db	361	MVSGCVPFPPSWK	PQOMPPEEPL	384	

RESULT 2

Q8N632	PRELIMINARY;	PRT;	470 AA.
ID	Q8N632		
AC	Q8N632;		
DT	01-OCT-2002	(TrEMBLrel. 22, Created)	
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)	
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)	
DE	Sphingosine kinase 1.		
GN	Name=SPHK1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood, and Skin;		
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bozak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		

```

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA EMBL; BC030553; AAH30553.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0046521; P:intracellular signaling cascade; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR001206; DAGKc.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKc; 1.
DR SMART; SM00046; DAGKc; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 470 AA; 51084 MW; 512E93A38C7CC17 CRC64;

Query Match 99.8%; Score 2013; DB 2; Length 470;
Best Local Similarity 99.7%; Pred. No. 9.5e-163;
Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQFRSHVQPLLAEEAIEISFTLMLTERRNHA 60
DB 87 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQFRSHVQPLLAEEAIEISFTLMLTERRNHA 146
QY 61 RELVRSEELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
DB 147 RELVRSEELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 206
QY 121 NHYAGVEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
DB 207 NHYAGVEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 266
QY 181 SEKYRRLGEMRFTLGTFLRLAALRYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240
DB 267 SEKYRRLGEMRFTLGTFLRLAALRYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 326
QY 241 LEEPVPVSHWTVVDEDFVLVLLHSHLGSEMPFAAPMGRCAGVMHLYFVRAGVSAMLL 300
DB 327 LEEPVPVSHWTVVDEDFVLVLLHSHLGSEMPFAAPMGRCAGVMHLYFVRAGVSAMLL 386
QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
DB 387 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 446
QY 361 MVSGCVPPEPPSWKPPQMPPEEPL 384
DB 447 MVSGCVPPEPPSWKPPQMPPEEPL 470

RESULT 3
Q96HV8 PRELIMINARY; PRT; 384 AA.
ID Q96HV8
AC Q96HV8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPHK1 protein.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA EMBL; BC008040; AAH08040.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:intracellular signaling cascade; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR001206; DAGKc.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKc; 1.
DR SMART; SM00046; DAGKc; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ SEQUENCE 384 AA; 42474 MW; F82999FF306113B0 CRC64;

Query Match 99.5%; Score 2006; DB 2; Length 384;
Best Local Similarity 99.5%; Pred. No. 2.9e-162;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQFRSHVQPLLAEEAIEISFTLMLTERRNHA 60
DB 1 MDPAGGPRGVLPRPCRVLLNPRGGKQKALQFRSHVQPLLAEEAIEISFTLMLTERRNHA 60
QY 61 RELVRSEELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
DB 61 RELVRSEELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
QY 121 NHYAGVEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
DB 121 NHYAGVEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
QY 181 SEKYRRLGEMRFTLGTFLRLAALRYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240
DB 181 SEKYRRLGEMRFTLGTFLRLAALRYRGLAYLPVGRVSKTPASPVVVOQGPVDAHLVP 240
QY 241 LEEPVPVSHWTVVDEDFVLVLLHSHLGSEMPFAAPMGRCAGVMHLYFVRAGVSAMLL 300
DB 241 LEEPVPVSHWTVVDEDFVLVLLHSHLGSEMPFAAPMGRCAGVMHLYFVRAGVSAMLL 300
QY 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360
DB 301 RLFLAMEKGRHMEYECPLYVVPVAFRLPKDGMFAVDGELMVSEAVQGVHPNYFW 360

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Db      301 RLFLAMEKGRHMEYECPLYVVPVAFRLPDKGKGVFAVDGELMVSEAVQGVHPNIFW 360
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Qy      361 MYSGCVPPEPPSWKPPQMPPEEPL 384
      |||
Db      361 MYSGCVPPEPPSWKPPQMPPEEPL 384
      |||

RESULT 4
Q96GK1 ID Q96GK1 PRELIMINARY; PRT; 398 AA.
AC DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sphingosine kinase 1.
GN Name=SPHK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009419; AAH09419.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:000287; F:magnesium ion binding; ISS.
DR GO; GO:0007287; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGK; 1.
DR SMART; SM00046; DAGK; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ SEQUENCE 398 AA; 43944 MW; 7F2C9B26C030E560 CRC64;

Query Match 99.0%; Score 1996; DB 2; Length 398;
Best Local Similarity 96.2%; Pred. No. 2.1e-161;
Matches 383; Conservative 1; Mismatches 0; Indels 14; Gaps 1;

Qy      1 MDP-----AGGPRGVLPFCRVLLNPRGGKQKALQLFRRSHVQPLLAAE 46
      |||
Db      1 MDPVVGCGRLFGFVFSAGGPRGVLPFCRVLLNPRGGKQKALQLFRRSHVQPLLAAE 60
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Qy      47 ISFTMLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVVGIMERPDPWETAIOKPLC 106
      |||
Db      61 ISFTMLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVVGIMERPDPWETAIOKPLC 120
      |||
Qy      107 SLPAGSGNALAASLNHYAGYEQVTNEDLLTNTCTLLCRRLSPNNLLSLHTASGLRLLFSV 166
      |||
Db      121 SLPAGSGNALAASLNHYAGYEQVTNEDLLTNTCTLLCRRLSPNNLLSLHTASGLRLLFSV 180
      |||
Qy      167 LSLAWGFIADVDESSEKRYRRLGEMRFTLTGTLRLAALRTYRGLAYLPLVGRVGSKTSPASP 226
      |||
Db      181 LSLAWGFIADVDESSEKRYRRLGEMRFTLTGTLRLAALRTYRGLAYLPLVGRVGSKTSPASP 240
      |||
Qy      227 VVVOGQPVDAHLVPLEPVPVSHWTVDPDEDVLVLLHSLGSEMFAAPNRCRCAAGVMH 286
      |||
Db      241 VVVOGQPVDAHLVPLEPVPVSHWTVDPDEDVLVLLHSLGSEMFAAPNRCRCAAGVMH 300
      |||
Qy      287 LFYVRAGVSRAMLRLFLAMEKGRHMEYECPLYVVPVAFRLPDKGKGVFAVDGELMV 346
      |||
Db      301 LFYVRAGVSRAMLRLFLAMEKGRHMEYECPLYVVPVAFRLPDKGKGVFAVDGELMV 360
      |||
Qy      347 SEAVQGVHPNYFWMVSGCVPPEPPSWKPPQMPPEEPL 384
      |||
Db      361 SEAVQGVHPNYFWMVSGCVPPEPPSWKPPQMPPEEPL 398
      |||

RESULT 5
Q9NOA5 ID Q9NOA5 PRELIMINARY; PRT; 329 AA.
AC DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Unnamed protein product.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046025; BAB01607.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001395; Aldo/ket_red.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGK; 1.
DR SMART; SM00046; DAGK; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ SEQUENCE 329 AA; 36393 MW; 7F430ABD0CA5FDC7 CRC64;

Query Match 81.5%; Score 1644; DB 2; Length 329;
Best Local Similarity 98.1%; Pred. No. 1.6e-131;
Matches 316; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MDPAGGPRGVLPFCRVLLNPRGGKQKALQLFRRSHVQPLLAAEISFTMLTERRNHA 60
      |||
Db      1 MDPAGGPRGVLPFCRVLLNPRGGKQKALQLFRRSHVQPLLAAEISFTMLTERRNHA 60
      |||
Qy      61 RELVRSEELGRWDALVVMGSDGLMHEVVGIMERPDPWETAIOKPLCSLPGSGNALAASL 120
      |||
Db      61 RELVRSEELGRWDALVVMGSDGLMHEVVGIMERPDPWETAIOKPLCSLPGSGNALAASL 120
      |||
Qy      121 NHYAGYEQVTNEDLLTNTCTLLCRRLSPNNLLSLHTASGLRLLFSVLAWGFIADVLE 180
      |||

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Db      121 NHYAGYEQVTNEDLLTNCRLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFADVDLE 180
QY      181 SKYRRLGEMRTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVPVVOQGPVDAHLVP 240
Db      181 SKYRRLGEMRTLTGTLFLAALRTYRGLAYLPVGRAGSKTPSPVPVVOQGPVDAHLVP 240
QY      241 LEEPVPSTWTVDPDEDVLVLALLSHLSEMFAPMGRCAAGVMHLPFVRAGVSRAMLL 300
Db      241 LEEPVPSTWTVDPDQDFVLVLALLSHLSEMFAPMGRCAAGVMHLPFVRAGVSRAMLL 300
QY      301 RLFLAMEKGRHMEYECPLYVYV 322
Db      301 RLFLAMEKGRHMEYECPLYVYI 322

RESULT 6
Q8CI15 PRELIMINARY; PRT; 382 AA.
AC Q8CI15;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sphingosine kinase 1.
GN Name=Sphk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMedID=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC037710; AAH37710.1; -.
DR MGD; MGI:1316649; Sphk1.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005824; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR InterPro; IPR001206; DAGKC.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
KW Kinase.
SQ SEQUENCE 382 AA; 42443 MW; B791FAA58FCE3D29 CRC64;

Query Match 81.1%; Score 1636.5; DB 2; Length 382;

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Best Local Similarity 80.7%; Pred. No. 8.4e-131;
Matches 309; Conservative 34; Mismatches 39; Indels 1; Gaps 1;

QY      1 MDPAGGRGVLPKRCRVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHA 60
Db      1 MEVVECPRGLLPKRCRVLLNPOGGKQKALQFRVQPFLEAEITFKLILTERKQHA 60
QY      61 RELVRSBELGRWDALVWMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db      61 RELVCAEELGHWDALVWMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASV 120
QY      121 NHYAGYEQVTNEDLLTNCRLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFADVDLE 180
Db      121 NHYAGYEQVTNEDLLTNCRLCRLLSPMNLSSLHTASGLRFLSVLSLAWGFADVDLE 180
QY      181 SEKVRRLGEMRTLTGTLFLAALRTYRGLAYLPVGRVSKTPASPVPVVOQGPVDAHLVP 240
Db      181 SEKVRRLGEMRTLTGTLFLAALRTYRGLAYLPVGTTVASKRPAS-TLVQKGPVDTHLVP 239
QY      241 LEEPVPSTWTVDPDEDVLVLALLSHLSEMFAPMGRCAAGVMHLPFVRAGVSRAMLL 300
Db      240 LEEPVPSTWTVDPDQDFVLVLALLSHLSEMFAPMGRCAAGVMHLPFVRAGVSRAMLL 299
QY      301 RLFLAMEKGRHMEYECPLYVYVVPVAPRLEPKDGKMFADGELMVSEAVQGVHPNFW 360
Db      300 RLFLAMQKQKEMELDCPLYVHVVPVAFRLEPRSQRGVFDGELMVCEAVQGVHPNVLW 359
QY      361 MVSGCVPEPPSPKQPMPPPEP 383
Db      360 MVGSRDAPSGRDSRRGPPPEP 382

RESULT 7
Q91ZN3 PRELIMINARY; PRT; 381 AA.
AC Q91ZN3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sphingosine kinase 1a.
GN Name=Sphk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Thompson D., Pyne S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF415213; AAL07499.1; -.
DR MGD; MGI:1316649; Sphk1.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005824; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKC; 1.
DR SMART; SM00046; DAGKC; 1.
KW Kinase.
SQ SEQUENCE 381 AA; 42344 MW; 2F2C1F10D59EB129 CRC64;

Query Match 80.7%; Score 1627.5; DB 2; Length 381;
Best Local Similarity 81.4%; Pred. No. 4.9e-130;
Matches 307; Conservative 33; Mismatches 36; Indels 1; Gaps 1;

QY      7 PRGVLPKRCRVLLNPRGGKQKALQFRSHVQPLLAEBEISFTLMLTERRNHARELVRS 66
Db      6 PRGLLPKRCRVLLNPOGGKQKALQFRVQPFLEAEITFKLILTERKQHAARELVCA 65
QY      67 RELGRWDALVWMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGY 126

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Db 66 BELGHWDALVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGNALAASVNHVAGY 125
 QY 127 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 186
 Db 126 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 185
 QY 187 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 246
 Db 186 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 244
 QY 247 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 306
 Db 245 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 304
 QY 307 EKGHRMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 366
 Db 305 QKGKHMELDCPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 364
 QY 367 EPPSPKQPMPPPEP 383
 Db 365 DAPSGRDRRGGPPPEP 381

RESULT 8

088886 PRELIMINARY; PRT; 388 AA.
 ID O88886
 AC O88886;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sphingosine kinase.
 GN Name=Sphk1; Synonyms=SPHK1b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98395082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722;
 RA Kohama T., Olivera A., Edsall L., Nagiec M.M., Dickson R., Spiegel S.;
 RT "Molecular cloning and functional characterization of murine
 RT sphingosine kinase."
 RL J. Biol. Chem. 273:23722-23728 (1998).
 DR EMBL; AF068749; AAC61698.1; -.
 DR MGD; MGI:1316649; Spk1.
 DR GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
 DR GO; GO:0007205; P:protein kinase C activation; IEA.
 DR InterPro; IPR001206; DAGKC.
 DR Pfam; PF00781; DAGK cat; 1.
 DR ProDom; PD005043; DAGKC; 1.
 DR SMART; SM00046; DAGKC; 1.
 KW Kinase.
 SQ SEQUENCE 388 AA; 43254 MW; 01EB032322542CAD CRC64;

Query Match 80.7%; Score 1627.5; DB 2; Length 388;
 Best Local Similarity 81.4%; Pred. No. 5e-130;
 Matches 307; Conservative 33; Mismatches 36; Indels 1; Gaps 1;

QY 7 PRGVLPKRCVLLNPRGGKQKALQLFQRSHVQPLLAEEISFTMLTERRNHARELVRS 66
 Db 13 PRGLLPKRCVLLNPRGGKQKALQLFQRSHVQPLLAEEISFTMLTERRNHARELVCA 72
 QY 67 BELGHWDALVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGNALAASVNHVAGY 126
 Db 73 BELGHWDALVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGNALAASVNHVAGY 132
 QY 127 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 186
 Db 133 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 192
 QY 187 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 246
 Db 193 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 251

QY 247 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 306
 Db 252 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 311
 QY 307 EKGHRMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 366
 Db 312 QKGKHMELDCPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 371
 QY 367 EPPSPKQPMPPPEP 383
 Db 372 DAPSGRDRRGGPPPEP 388

RESULT 9

088885 PRELIMINARY; PRT; 504 AA.
 ID O88885
 AC O88885;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sphingosine kinase (Fragment).
 GN Name=Sphk1; Synonyms=SPHK1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98395082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722;
 RA Kohama T., Olivera A., Edsall L., Nagiec M.M., Dickson R., Spiegel S.;
 RT "Molecular cloning and functional characterization of murine
 RT sphingosine kinase."
 RL J. Biol. Chem. 273:23722-23728 (1998).
 DR EMBL; AF068748; AAC61697.1; -.
 DR MGD; MGI:1316649; Spk1.
 DR GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
 DR GO; GO:0007205; P:protein kinase C activation; IEA.
 DR InterPro; IPR001206; DAGKC.
 DR Pfam; PF00781; DAGK cat; 1.
 DR ProDom; PD005043; DAGKC; 1.
 DR SMART; SM00046; DAGKC; 1.
 KW Kinase.
 FT NON TER
 SQ SEQUENCE 504 AA; 55119 MW; 2AAFEBA72027F509 CRC64;

Query Match 80.5%; Score 1624.5; DB 2; Length 504;
 Best Local Similarity 81.2%; Pred. No. 1.3e-129;
 Matches 306; Conservative 34; Mismatches 36; Indels 1; Gaps 1;

QY 7 PRGVLPKRCVLLNPRGGKQKALQLFQRSHVQPLLAEEISFTMLTERRNHARELVRS 66
 Db 129 PRGLLPKRCVLLNPRGGKQKALQLFQRSHVQPLLAEEISFTMLTERRNHARELVCA 188
 QY 67 BELGHWDALVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGNALAASVNHVAGY 126
 Db 189 BELGHWDALVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGNALAASVNHVAGY 248
 QY 127 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 186
 Db 249 EQVTNEDLLTNTCTLLCRRLSPMNLISLHTASGLRLFSVLISLAWGFTADVLDSEKYYR 308
 QY 187 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 246
 Db 309 LGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSKTTPASPVVVOGPPVDLHVLPLEEVP 367
 QY 247 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 306
 Db 368 SHHTVVPDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 427
 QY 307 EKGHRMEYECPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 366
 Db 428 QKGKHMELDCPLYVVPVAVFRLEPKDGKGMFAVDGELMVSEAVQGVHFNFMVSGCV 487

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QY 367 EPPPSKQOMPPPEP 383
Db 488 DAPSGRDRGPPPEP 504

RESULT 10
Q642F6 PRELIMINARY; PRT; 383 AA.
AC Q642F6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Sphingosine kinase 1.
GN Name=Sphki;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081738; AAH81738.1; -.
KW Kinase.
SQ SEQUENCE 383 AA; 42432 MW; 70B6E217AF812F77 CRC64;

Query Match 79.3%; Score 1599.5; DB 2; Length 383;
Best Local Similarity 78.1%; Pred. No. 1.2e-127;
Matches 300; Conservative 42; Mismatches 41; Indels 1; Gaps 1;

QY 1 MDPAGPRGLVLPKCRVLVLLNPRGKGKALQIFRSHVQPLLAEEISFTMLTERRNHA 60
Db 1 MQPADCPRGLLPKCRVLVLLNPRGKGKALQIFQSRVRLLEAEVSPKMLTERQNH 60
QY 61 RELVRSSELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVCAEELGHWDALAVMSGDGLMHEVNVNGLMERPDWESAIQKPLCSLPAGSGNALAASL 120
QY 121 NYAGVQVNTNEDLLTNCITLLCRLLSPMNLISLHTASGLRIFSVLSLAWGFADVDLE 180
Db 121 NYAGHEQVNTNEDLLTNCITLLCCRQLSPMNLISLHTASGRQLYSVLSLWGFADVDLE 180
QY 181 SEKYRRLGEMRFTLTGTFRLAALRTYGRGLAYLIPVGRVSGKTPASPVVVOQGPDVADHLP 240
Db 181 SEKYRSLGEIRFTVGTFFRLASLRIYQQLAYLIPVGAASKIPASS-LAQKGPANTYLP 239
QY 241 LEEPVPSHWTVPPDEDFVLVLLHSHLGSEMFAPMGRCACAGVMHLFYVRAGVSRAML 300
Db 241 LEEPVPHTWTVPEQDFVLVLLHSHLGSEMFAPMGRCACAGVMHLFYVRAGVSRAML 300
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Db 240 LEEVPVPHWTVPPQDFVLVLLHSHLGSEMFAPMGRCACAGVMHLFYVRAGVSRAML 299
QY 301 RLFLAMEKGRHMEYECPLVYVPAFRLEBPKCKGMFAVDGELMWSEAVOGQVHPNYFW 360
Db 300 RLFLAMQGRHMDLDCPLVYVPAFRLEBPNRGVFSVDGELMWCEAVOGQVHPNYLW 359
QY 361 MVSGCVPPEPPSWKQPMPPPEPL 384
Db 360 MVSGSSDPSGRDSQRRPPPEPI 383

RESULT 11
Q91V26 PRELIMINARY; PRT; 383 AA.
AC Q91V26;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Sphingosine kinase 1f (Sphingosine kinase 1a) (Sphingosine kinase 1c)
DE (Sphingosine kinase 1d) (Sphingosine kinase 1e).
GN Name=sphk1f; Synonyms=sphkia, sphk1c, sphk1d, sphk1e;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Imamura T., Ohtane J., Ito S., Ogawa T., Hattori N., Tanaka S.,
RA Shiota K.;
RT "CpG island of rat sphingosine kinase-1 gene: tissue-dependent DNA
RT methylation status and multiple alternative first exons.";
RL Genomics 78:117-125(2001).
DR EMBL; AB049575; BAB62324.1; -.
DR EMBL; AB049571; BAB62320.1; -.
DR EMBL; AB049572; BAB62321.1; -.
DR EMBL; AB049573; BAB62322.1; -.
DR EMBL; AB049574; BAB62323.1; -.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
DR GO; GO:0000287; F:magnesium ion binding; ISS.
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR GO; GO:0046521; P:sphingoid catabolism; ISS.
DR Pfam; PF00781; DAGK_cat; 1.
DR ProDom; PD005043; DAGKc; 1.
DR SMART; SM00046; DAGKc; 1.
KW Kinase.
SQ SEQUENCE 383 AA; 42418 MW; CAAD5817BF4B9507 CRC64;

Query Match 79.2%; Score 1596.5; DB 2; Length 383;
Best Local Similarity 77.9%; Pred. No. 2.2e-127;
Matches 299; Conservative 43; Mismatches 41; Indels 1; Gaps 1;

QY 1 MDPAGPRGLVLPKCRVLVLLNPRGKGKALQIFRSHVQPLLAEEISFTMLTERRNHA 60
Db 1 MQPADCPRGLLPKCRVLVLLNPRGKGKALQIFQSRVRLLEAEVSPKMLTERQNH 60
QY 61 RELVRSSELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVCAEELGHWDALAVMSGDGLMHEVNVNGLMERPDWESAIQKPLCSLPAGSGNALAASL 120
QY 121 NYAGVQVNTNEDLLTNCITLLCRLLSPMNLISLHTASGLRIFSVLSLAWGFADVDLE 180
Db 121 NYAGHEQVNTNEDLLTNCITLLCCRQLSPMNLISLHTASGRQLYSVLSLWGFADVDLE 180
QY 181 SEKYRRLGEMRFTLTGTFRLAALRTYGRGLAYLIPVGRVSGKTPASPVVVOQGPDVADHLP 240
Db 181 SEKYRSLGEIRFTVGTFFRLASLRIYQQLAYLIPVGAASKIPASS-LAQKGPANTYLP 239
QY 241 LEEPVPSHWTVPPDEDFVLVLLHSHLGSEMFAPMGRCACAGVMHLFYVRAGVSRAML 300
Db 240 LEEPVPHTWTVPEQDFVLVLLHSHLGSEMFAPMGRCACAGVMHLFYVRAGVSRAML 299
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QY 301 RLFLAMEGRHMEYPCYLYVVPVAVFRLPKDGGKMGFAVDGELMVSEAVQGVHPNFV 360
DB 300 RLFLAQKQKGMDDLPCLYLVHVPVAVFRLPNRQGVFSDGELMVCEAVQGVHPNFV 359
QY 361 MYSGCVPEPPSPKQPMQPPPEPL 384
DB 360 MYSGSDSPSGRDSQRRPPPEPI 383

RESULT 12
Q9BTG7 PRELIMINARY; PRT; 287 AA.
AC Q9BTG7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPHK1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez A., Rodriguez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004112; AA04112.2; -.
DR GO; GO:0004143; F:diacylglycerol kinase activity; IEA.
DR GO; GO:0007205; P:protein kinase C activation; IEA.
DR InterPro; IPR001206; DAKGC.
DR Prodom; PD005043; DAKGC; 1.
FT NON_TER 1
SQ SEQUENCE 287 AA; 31684 MW; 2A0FDD51B64982C7 CRC64;

Query Match 74.6%; Score 1505; DB 2; Length 287;
Best Local Similarity 99.7%; Pred. No. 9,3e-120;
Matches 286; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 98 ETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCRLSPMNLSSLHT 157
DB 1 ETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCRLSPMNLSSLHT 60

QY 158 ASGLRFLSVLSAWGFADVDLSEKRYRLGEMRFTGLTFLAALRYRGLAYLPVGR 217
DB 61 ASGLRFLSVLSAWGFADVDLSEKRYRLGEMRFTGLTFLAALRYRGLAYLPVGR 120

QY 218 VGSKTPASPVVQGVDAHLVPLEPVPVSHWTVDPDEDVFLVLALLSHLSEMPAAM 277

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DB 121 VGSKTPASPVVQGVDAHLVPLEPVPVSHWTVDPDEDVFLVLALLSHLSEMPAAM 180
QY 278 GRCAAGVMHLFYTRAGVSRAMLRLFLAMEKGRHMEYCEPYLYVVPVAVFRLPKDQKGM 337
DB 181 GRCAAGVMHLFYTRAGVSRAMLRLFLAMEKGRHMEYCEPYLYVVPVAVFRLPKDQKGV 240
QY 338 FAVDGLMVSEAVQGVHPNFVFMVSGCVPEPPSPKQPMQPPPEPL 384
DB 241 FAVDGLMVSEAVQGVHPNFVFMVSGCVPEPPSPKQPMQPPPEPL 287

RESULT 13
SPH2_MOUSE
ID SPH2_MOUSE STANDARD; PRT; 617 AA.
AC Q9UIA7; Q91VA9; Q9DBH6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE SPHK1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=22347850; PubMed=10751414; DOI=10.1074/jbc.M002759200;
RA Liu H., Sugtara M., Nava V.E., Edsall L.C., Kono K., Poulton S.,
RA Milstien S., Kohama T., Spiegel S.;
RT "Molecular cloning and functional characterization of a novel
RT mammalian sphingosine kinase type 2 isoform.";
RL J. Biol. Chem. 275:19513-19520 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Thompson D., Pyne S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.

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RC TISSUE-Limb, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters K.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Catalyzes the phosphorylation of sphingosine to form
sphingosine 1-phosphate (SPP), a lipid mediator with both intra-
and extracellular functions. Also acts on D-erythro-
dihydrospingosine, D-erythro-sphingosine and L-threo-
dihydrospingosine.
CC dihydrospingosine.
CC -!- CATALYTIC ACTIVITY: Sphingosine + ATP = sphingosine 1-phosphate +
ADP.
CC -!- SIMILARITY: Contains 1 DAGKc domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC ENBL; AF245448; AAF74125.1; -
DR ENBL; AF415214; AAL07500.1; -
DR ENBL; AK004951; BAB23694.1; -
DR ENBL; BC006941; AAK06941.1; -
DR ENBL; BC053737; AAK53737.1; -
DR MGD; MGI:1861380; Sphk2.
DR GO; GO:0005829; C:cytosol; IEP.
DR GO; GO:0005624; C:membrane fraction; IEP.
DR GO; GO:0017050; F:D-erythro-sphingosine kinase activity; IDA.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0017016; F:Ras interactor activity; ISS.
DR GO; GO:0008481; F:sphinganine kinase activity; NAS.
DR GO; GO:0006916; P:anti-apoptosis; NAS.
DR GO; GO:0008283; P:cell proliferation; NAS.
DR GO; GO:0006669; P:sphinganine-1-phosphate biosynthesis; NAS.
DR InterPro; IPR001206; DAGKc.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00781; DAGK cat; 1.
DR ProDom; PD005043; DAGKc; 1.
KW ATP-binding; Kinase; Transferase.
FT CONFLICT 252 252 N -> S (in Ref. 1).
FT CONFLICT 510 510 P -> T (in Ref. 1).
FT CONFLICT 548 548 L -> F (in Ref. 1).
SQ SEQUENCE 617 AA; 65618 MW; 40EE2C2C28B8E26A CRC64;
Query Match 44.38; Score 893; DB 1; Length 617;
Best Local Similarity 39.98; Pred. No. 3.3e-67;
Matches 192; Conservative 60; Mismatches 109; Indels 120; Gaps 5;
QY 10 VLPKPCRVLLNPRGKGKALQLFRSHVQFLAAEAEISFTMLTERRNHARELVSEEL 69
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QY 70 GRWDALVVMGDDGLMHVENVGLMERPDWETAIQKPLCLSPAGSGNALAASLNHYAGVEQV 129

Db 201 SEWEGIVTVSGDGLLYEVINGLLDRPOWEDAVRMPIGVLPCGSGNALAGAVNHHGGFEQV 260
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Db 261 VGVLLNCSLLCGSGHPLJDLUSVTLASGRCFSLSVANGFLSDVDIHSERFRALGS 320
QY 190 MRFTLGTFLRLAALRTYRGLAYLPV----- 215
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QY 216 -----GRVGS----- 220
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Db 501 E-FVLMGILPSHLCADLMAAPHARFDDGVVHLCWVRSGISRAALLRILLAMEHGNHFSL 559
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Db 560 GCPHLGYAARAARFRLPLEPLTPRGLLTVDGELVEYGPQAVHPGLATLLTG-----PAGQKP 615
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DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2] SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 11:56:47 ; Search time 43 Seconds
(without alignments)
666.634 Million cell updates/sec

Title: US-10-642-289-2
Perfect score: 2017
Sequence: 1 MDPAGPRGVLPKPCRLVL.....CVERPPSWKPPQMPPEBPL 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2017	100.0	384	4	US-09-959-897-2
2	2013	99.8	384	4	US-09-970-516-2
3	2005	99.4	384	4	US-09-949-016-7026
4	2005	99.4	384	4	US-09-796-487-3
5	1920	95.2	368	4	US-10-053-510-21
6	1639	81.3	312	4	US-09-949-016-9811
7	1629.5	80.8	382	4	US-09-970-516-6
8	1627.5	80.7	388	4	US-09-817-676A-15
9	1627.5	80.7	388	4	US-09-796-487-2
10	1624.5	80.5	381	4	US-09-796-487-1
11	1624.5	80.5	381	4	US-09-796-487-4
12	1606.5	79.6	373	4	US-09-796-487-5
13	1538	76.3	293	4	US-09-205-258-328
14	935.5	46.4	204	4	US-09-796-487-9
15	894	43.8	617	4	US-09-817-676A-12
16	883.5	43.8	618	4	US-09-970-516-4
17	883.5	43.8	618	4	US-09-817-676A-14
18	560	27.8	490	4	US-10-053-510-19
19	519.5	25.8	524	4	US-10-053-510-20
20	453	22.5	119	4	US-09-205-258-788
21	375	18.6	392	4	US-09-796-487-6
22	357.5	17.7	424	4	US-09-796-487-8
23	346	17.2	403	4	US-09-796-487-7
24	330	16.4	536	4	US-09-248-796A-15859
25	295	14.6	63	4	US-09-959-897-13
26	295	14.6	63	4	US-09-959-897-21
27	280	13.9	69	4	US-09-959-897-11

28	249	12.3	52	4	US-09-959-897-10	Sequence 10, Appl
29	249	12.3	52	4	US-09-959-897-18	Sequence 18, Appl
30	239	11.8	359	4	US-09-270-767-46720	Sequence 46720, A
31	239	11.8	687	4	US-09-270-767-45874	Sequence 45874, A
32	234	11.6	53	4	US-09-959-897-12	Sequence 12, Appl
33	234	11.6	53	4	US-09-959-897-20	Sequence 20, Appl
34	216	10.7	46	4	US-09-959-897-15	Sequence 15, Appl
35	216	10.7	46	4	US-09-959-897-23	Sequence 23, Appl
36	201	10.0	47	4	US-09-959-897-14	Sequence 14, Appl
37	201	10.0	47	4	US-09-959-897-22	Sequence 22, Appl
38	184	9.1	47	4	US-09-959-897-9	Sequence 9, Appl
39	184	9.1	54	4	US-09-959-897-17	Sequence 17, Appl
40	180.5	8.9	142	4	US-09-270-767-45594	Sequence 45594, A
41	180	8.9	144	4	US-09-270-767-33894	Sequence 33894, A
42	180	8.9	144	4	US-09-270-767-49111	Sequence 49111, A
43	170	8.4	49	4	US-09-959-897-16	Sequence 16, Appl
44	170	8.4	49	4	US-09-959-897-24	Sequence 24, Appl
45	162	8.0	372	4	US-09-603-208A-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-09-959-897-2
; Sequence 2, Application US/09959897
; Patent No. 6730480
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BAMBLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/09/959,897
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-897-2

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Best Local Similarity	100.0%;	Pred. No.	4.7e-219;	Mismatches	0;	Indels	0;
Matches	384;	Conservative	0;	Gaps	0;		
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Db	181	SEKYRELGEWRTTCTGTFLELALRTYRGVSKTPASPVVVOQGPVDHLYP	240				
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Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 2
US-09-970-516-2
; Sequence 2, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-516-2

Query Match 99.8%; Score 2013; DB 4; Length 384;
Best Local Similarity 99.7%; Pred. No. 1.3e-218;
Matches 383; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 361 MVSGCVPPEPPSWKPPQMPPEEPL 384

RESULT 3
US-09-949-016-7026
; Sequence 7026, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7026
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7026

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Matches 380; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4
US-09-796-487-3
; Sequence 3, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Spingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(384)
; OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspo
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; OTHER INFORMATION: nding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of Ge		Query Match		95.2%; Score 1920; DB 4; Length 368;
; OTHER INFORMATION: nBank sequence Accession Number AAF73423.		Best Local Similarity		99.7%; Pred. No. 4.1e-208;
; PUBLICATION INFORMATION:		Matches 367; Conservative		1; Mismatches 0; Indels 0; Gaps 0;
; AUTHORS: Nava et al.		QY		17 VLVLNPRGGKALQOLFRSHVQPLLAABEISFTMLTERENHARELVRSEELGRWDALV 76
; TITLE: Functional characterization of human spingosine kinase-1		Db		1 VLVLNPRGGKALQOLFRSHVQPLLAABEISFTMLTERENHARELVRSEELGRWDALV 60
; JOURNAL: FEBS Lett.		QY		77 VMSGDGLMHEVVGMLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
; VOLUME: 473		Db		61 VMSGDGLMHEVVGMLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120
; ISSUE: 1		QY		137 NCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKRYRRLGEMFTLGT 196
; PAGES: 81-84		Db		121 NCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKRYRRLGEMFTLGT 180
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; DATE: 2000		Db		181 FLRLAALTYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVPLEEPVPSHWTVPDED 240
; DATABASE ENTRY DATE: 2000-06-01		QY		257 FVLVLLALHSHLGSMPFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 316
; RELEVANT RESIDUES: (1)...		Db		241 FVLVLLALHSHLGSMPFAAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 300
; PUBLICATION INFORMATION:		QY		317 PYLVTVVPAFRLEPKDGKGMFAVDGELMVSEAVQGVHPNYFMVSGCVPBPSPKPOQ 376
; DATABASE ACCESSION NUMBER: AAF73423		Db		301 PYLVTVVPAFRLEPKDGKGMFAVDGELMVSEAVQGVHPNYFMVSGCVPBPSPKPOQ 360
; DATE: 2000-06-01		QY		377 MPPPEPL 384
; RELEVANT RESIDUES: (1)...		Db		361 MPPPEPL 368
US-09-796-487-3		RESULT 6		
Query Match		US-09-949-016-9811		
Best Local Similarity		; Sequence 9811, Application US/09949016		
Matches 380; Conservative		; Patent No. 6812339		
99.4%; Score 2005; DB 4; Length 384;		; GENERAL INFORMATION:		
3; Mismatches 1; Indels 0; Gaps 0;		; APPLICANT: VENTER, J. Craig et al.		
QY		; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED		
1	MDPAGGPRGVLPRPCRVLLNPRGGKALQOLFRSHVQPLLAABEISFTMLTERNHA 60	; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF		
Db	1 MDPAGGPRGVLPRPCRVLLNPRGGKALQOLFRSHVQPLLAABEISFTMLTERNHA 60	; FILE REFERENCE: CL001307		
QY	61 RELVRSEELGRWDALVMSGDGLMHEVVGMLMERPDWETAIQKPLCSLPAGSGNALAASL 120	; CURRENT APPLICATION NUMBER: US/09/949,016		
Db	61 RELVRSEELGRWDALVMSGDGLMHEVVGMLMERPDWETAIQKPLCSLPAGSGNALAASL 120	; PRIOR FILING DATE: 2000-04-14		
QY	121 NHYAGYEQVTNEDLLNCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180	; PRIOR APPLICATION NUMBER: 60/241,755		
Db	121 NHYAGYEQVTNEDLLNCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180	; PRIOR FILING DATE: 2000-10-20		
QY	181 SEKRYRRLGEMFTLGTFLRLAALTYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240	; PRIOR APPLICATION NUMBER: 60/237,768		
Db	181 SEKRYRRLGEMFTLGTFLRLAALTYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240	; PRIOR FILING DATE: 2000-10-03		
QY	241 LEEPVFVSHWTVPDEDVFLVLLALHSHLGSMPFAAPMGRCAAGVMHLFYVRAGVSRAML 300	; PRIOR APPLICATION NUMBER: 60/231,498		
Db	241 LEEPVFVSHWTVPDEDVFLVLLALHSHLGSMPFAAPMGRCAAGVMHLFYVRAGVSRAML 300	; NUMBER OF SEQ ID NOS: 207012		
QY	301 RLFLAMEKGRHMEYECPYLVVPAFRLEPKDGKGMFAVDGELMVSEAVQGVHPNYFV 360	; SOFTWARE: FastSeq for Windows Version 4.0		
Db	301 RLFLAMEKGRHMEYECPYLVVPAFRLEPKDGKGMFAVDGELMVSEAVQGVHPNYFV 360	; SEQ ID NO 9811		
QY	361 MVSGCVPBPSPKPOQMPPEPL 384	; LENGTH: 312		
Db	361 MVSGCVPBPSPKPOQMPPEPL 384	; TYPE: PRT		
RESULT 5		; ORGANISM: Human		
US-10-053-510-21		US-09-949-016-9811		
; Sequence 21, Application US/10053510		Query Match		81.3%; Score 1639; DB 4; Length 312;
; Patent No. 6830881		Best Local Similarity		99.7%; Pred. No. 1.8e-176;
; GENERAL INFORMATION:		Matches 311; Conservative		1; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Saba, Julie D.		QY		73 DALVVMGDLMEHVVGMLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNE 132
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,		Db		1 DALVVMGDLMEHVVGMLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNE 60
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND		QY		133 DLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKRYRRLGEMRF 192
; TITLE OF INVENTION: METHODS OF USE THEREFOR		Db		61 DLLTNTCTLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFADVDLSEKRYRRLGEMRF 120
; FILE REFERENCE: 200116.402C2		QY		193 TLGTFLRLAALTYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVPLEEPVPSHWTVV 252
; CURRENT APPLICATION NUMBER: US/10/053,510		Db		121 TLGTFLRLAALTYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVPLEEPVPSHWTVV 180
; CURRENT FILING DATE: 2002-01-17				
; NUMBER OF SEQ ID NOS: 21				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 21				
; LENGTH: 368				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-10-053-510-21				

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QY 253 PDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHM 312
Db 181 PDEDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHM 240
QY 313 EYECPLVTVVVFARLEPKDGKGFVAVDGLMVSEAVQGVHPNYFMVSGCVBPSPSW 372
Db 241 EYECPLVTVVVFARLEPKDGKGFVAVDGLMVSEAVQGVHPNYFMVSGCVBPSPSW 300
QY 373 KPQOMPPPEPL 384
Db 301 KPQOMPPPEPL 312

RESULT 7
US-09-970-516-6
; Sequence 6, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: polynucleotides encoding sphingosine kinases
; CURRENT FILING DATE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-970-516-6

Query Match 80.8%; Score 1629.5; DB 4; Length 382;
Best Local Similarity 80.4%; Pred. No. 3e-175;
Matches 308; Conservative 34; Mismatches 40; Indels 1; Gaps 1;

QY 1 MDPAGGPRGVLPQRCVLVLLNPRGGKQKALQLFRRSHVQPLLAEBAEISFTMLTERRNHA 60
Db 1 MEPVCPRGLLPQRCVLVLLNPRGGKQKALQLFQSRVQPFLEAEITFKLILTERKHA 60
QY 61 RELVSEELGRWDALVVMGSDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
Db 61 RELVCAEELGHDALVAMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASV 120
QY 121 NHYAGYEQVTNEDLLTNCTLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
Db 121 NHYAGYEQVTNEDLLTNCTLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLE 180
QY 181 SEKYRRLGEMRPTLGTFLRLAALRYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVP 240
Db 181 SEKYRRLGEMRPTLGTFLRLAALRYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVP 239
QY 241 LEEPVPSTWTVVPEQDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAML 300
Db 240 LEEPVPSTWTVVPEQDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAML 299
QY 301 RLFLAMEKGRHMEYECPLVTVVVFARLEPKDGKGFVAVDGLMVSEAVQGVHPNYFW 360
Db 300 RLFLAMEKGRHMEYECPLVTVVVFARLEPKDGKGFVAVDGLMVSEAVQGVHPNYFW 359
QY 361 MVSGCVBPSPSWKPQOMPPPEEP 383
Db 360 MVSGCVBPSPSWKPQOMPPPEEP 382

RESULT 8
US-09-817-676A-15
; Sequence 15, Application US/09817676A
; Patent No. 6800470
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Kohama, Takafumi
```

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; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; TITLE OF INVENTION: Expression and Methods of Use Thereof
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/194,318
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; TITLE: Molecular cloning and functional characterization of
; TITLE: murine sphingosine kinase
; JOURNAL: J. Biol. Chem.
; VOLUME: 273
; ISSUE: 37
; PAGES: 23722-23728
; DATE: 1998-09-11
; DATABASE ACCESSION NUMBER: AAC61698
; DATABASE ENTRY DATE: 1998-09-26
US-09-817-676A-15

Query Match 80.7%; Score 1627.5; DB 4; Length 388;
Best Local Similarity 81.4%; Pred. No. 5.2e-175;
Matches 307; Conservative 33; Mismatches 36; Indels 1; Gaps 1;

QY 7 PRGVLPRPCRVLLNPRGGKQKALQLFRRSHVQPLLAEBAEISFTMLTERRNHARELVRS 66
Db 13 PRGVLPRPCRVLLNPRGGKQKALQLFQSRVQPFLEAEITFKLILTERRNHARELVCA 72
QY 67 BELGRDALVVMGSDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
Db 73 BELGHDALVAMSGDGLMHEVNGLMERPDWETAIQKPLCSLPAGSGNALAASVNHYAGY 132
QY 127 EQVTNEDLLTNCTLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLESEKYRR 186
Db 133 EQVTNEDLLTNCTLLCRRLSPMNLISLHTASGLRFLSVLSLAWGFADVDLESEKYRR 192
QY 187 LGEMRFTLGTFLRLAALRYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVLEPVP 246
Db 193 LGEMRFTLGTFLRLAALRYRGLAYLPVGRVGSKTPASPVVVOQGPVDAHLVLEPVP 251
QY 247 SHWTVVPEQDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 306
Db 252 SHWTVVPEQDFVLVLLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAM 311
QY 307 EKGHRMEYECPLVTVVVFARLEPKDGKGFVAVDGLMVSEAVQGVHPNYFMVSGCV 366
Db 312 QKGKHELDPCPLVHVPVAFRLPRSRQGVFSDGELMVCEAVQGVHPNYLMMVCGSR 371
QY 367 EPPPSWKPPQMPPEEP 383
Db 372 DAPSGRDSRRGPPPEEP 388

RESULT 9
US-09-796-487-2
; Sequence 2, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
```

SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 388
TYPE: PRT
ORGANISM: Mus Musculus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(388)
OTHER INFORMATION: SEQ ID NO 2 is the peptide sequence of SPHK1b in Fig. 1, corresponding to amino acid residue 1 to 388 of SPHK1b of GenBank sequence AAC61697.
OTHER INFORMATION: e Accession Number AAC61697.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
TITLE: Molecular cloning and functional characterization of murine sphingosine kinase
JOURNAL: Journal of Biological Chemistry
VOLUME: 273
ISSUE: 37
PAGES: 23722-23728
DATE: 1998
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1)-(388)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1)-(388)
US-09-796-487-2

Query Match 80.7%; Score 1627.5; DB 4; Length 388;
Best Local Similarity 81.4%; Pred. No. 5.2e-175;
Matches 307; Conservative 33; Mismatches 36; Indels 1; Gaps 1;
QY 7 PRGLPRPCRVLLNPNQGGKQKALQFRSHVQPLLAELAEISFTLMLTERRNHARELVRS 66
Db 13 PRGLPRPCRVLLNPNQGGKQKALQFRSHVQPLLAELAEISFTLMLTERRNHARELVCA 72
QY 67 BELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
Db 73 BELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 132
QY 127 EQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVSLWAGFIADVDLESEKYRR 186
Db 133 EQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVSLWAGFIADVDLESEKYRR 192
QY 187 LGEMRTFLGTFLRLAALRTYRGRLAYLPVGRVSKTPASPVVVOQGPVDAHLVPLEEPVP 246
Db 193 LGEMRTFLGTFLRLAALRTYRGRLAYLPVGRVSKTPASPVVVOQGPVDAHLVPLEEPVP 251
QY 247 SHWTVVPDEDFVLVLLHSLHSGEMFAAPMGRCAGVMHFLFYVRAGVSRAMLRLFLAM 306
Db 252 SHWTVVPDEDFVLVLLHSLHSGEMFAAPMGRCAGVMHFLFYVRAGVSRAMLRLFLAM 311
QY 307 EKGHRMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHFNFMVSGCV 366
Db 312 EKGHRMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHFNFMVSGCV 371
QY 367 EPPPSWKPKQMPPEEP 383
Db 372 DAPSGRDSRRGPPPEEP 398

RESULT 10
US-09-796-487-1
Sequence 1, Application US/09796487
Patent No. 6830916
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosine Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 0732001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/530,868
PRIORITY DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 381
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(381)
OTHER INFORMATION: SEQ ID NO 1 is the peptide sequence of SPHK1a in Figure 1, corresponding to amino acid residue 124 to 504 of SPHK1a of GenBank sequence AAC61697. SEQ ID NO 1 is equivalent to SEQ ID NO 4 that is the amino acid sequence of mSPHK1a in Figure 3.
OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHK1a in Figure 3.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
TITLE: Molecular cloning and functional characterization of murine sphingosine kinase
JOURNAL: Journal of Biological Chemistry
VOLUME: 237
ISSUE: 37
PAGES: 23722-23728
DATE: 1998
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)-(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)-(504)
US-09-796-487-1

Query Match 80.5%; Score 1624.5; DB 4; Length 381;
Best Local Similarity 81.2%; Pred. No. 1.1e-174;
Matches 306; Conservative 34; Mismatches 36; Indels 1; Gaps 1;
QY 7 PRGLPRPCRVLLNPNQGGKQKALQFRSHVQPLLAELAEISFTLMLTERRNHARELVRS 66
Db 6 PRGLPRPCRVLLNPNQGGKQKALQFRSHVQPLLAELAEISFTLMLTERRNHARELVCA 65
QY 67 BELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
Db 66 BELGRWDALVMSGDGLMHEVNVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 125
QY 127 EQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVSLWAGFIADVDLESEKYRR 186
Db 126 EQVTNEDLLTNCITLLCRRLSPMNLISLHTASGLRSLFVSLWAGFIADVDLESEKYRR 185
QY 187 LGEMRTFLGTFLRLAALRTYRGRLAYLPVGRVSKTPASPVVVOQGPVDAHLVPLEEPVP 246
Db 186 LGEMRTFLGTFLRLAALRTYRGRLAYLPVGRVSKTPASPVVVOQGPVDAHLVPLEEPVP 244
QY 247 SHWTVVPDEDFVLVLLHSLHSGEMFAAPMGRCAGVMHFLFYVRAGVSRAMLRLFLAM 306
Db 245 SHWTVVPDEDFVLVLLHSLHSGEMFAAPMGRCAGVMHFLFYVRAGVSRAMLRLFLAM 304
QY 307 EKGHRMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHFNFMVSGCV 366
Db 305 EKGHRMEYECPLYVYVVAFLRLEPKDGMFAVDGELMVSEAVQGVHFNFMVSGCV 364
QY 367 EPPPSWKPKQMPPEEP 383
Db 365 DAPSGRDSRRGPPPEEP 391

RESULT 11
US-09-796-487-4
Sequence 4, Application US/09796487
Patent No. 6830916
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah

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; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(381)
; OTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of mSPHK1a in Figure 3, corre
; OTHER INFORMATION: sponding to amino acid residue 124 to 504 of SPHK1a of GenBank se
; OTHER INFORMATION: quence Accession Number AF068748. SEQ ID NO 4 is equivalent to SE
; OTHER INFORMATION: Q ID NO 1 that is the amino acid sequence of SPHK1a in Figure 1.
; PUBLICATION INFORMATION:
; AUTHORS: Kohama et al.,
; TITLE: Molecular cloning and functional characterization of murine sphingosine
; TITLE: kinase
; JOURNAL: Journal of Biological Chemistry
; VOLUME: 273
; ISSUE: 37
; PAGES: 23722-23728
; DATE: 1998
; DATABASE ACCESSION NUMBER: AAC61697
; DATABASE ENTRY DATE: 1998-09-26
; RELEVANT RESIDUES: (124)..(504)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC61697
; DATABASE ENTRY DATE: 1998-09-26
; RELEVANT RESIDUES: (124)..(504)
US-09-796-487-4

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Query Match      80.5%; Score 1624.5; DB 4; Length 381;
Best Local Similarity 81.2%; Pred. No. 1.1e-174;
Matches 306; Conservative 34; Mismatches 36; Indels 1; Gaps 1;

Qy 7 PRGVLPKRCVLLVLPNGGKGKALQLFRSHVQPLLAAEABISFTMLTERNNHARELVRS 66
Db 6 PRGLLPKRCVLLVLPNGGKGKALQLFQSRVQPFLEAEITFKLILTERKNHARELVCA 65

Qy 67 BELGRWDALVVMGSGDGLMHVVGNGLMERPDPWETAIOKPLCSLPAGSGNALAASLNHYAGY 126
Db 66 BELGHWDAVVMGSGDGLMHVVGNGLMERPDPWETAIOKPLCSLPAGSGNALAASLNHYAGY 125

Qy 127 EQVTNEDLLTCTLLCRRLLSPMNLISHTASGLRFLSVLSLAWGFTIADVDLSEKYYR 186
Db 126 EQVTNEDLLTCTLLCRRLLSPMNLISHTASGLRFLSVLSLAWGFTIADVDLSEKYYR 185

Qy 187 LGEMRFTLGTFLRLAALRTYGRILAYLPVGRVSKTPASPVVQGGPVDLHLPLEPVP 246
Db 186 LGEMRFTVGTFFRLASRLIYQGLAYLPVGTVAKRPPAS-TLVQKGPVDTHLVPLEPVP 244

Qy 247 SHWTVVPDDEFLVLALAHSLGSEMPAAMPGRCAAGVMHLFYVRAGVSRAMLRLFLAM 306
Db 245 SHWTVVPDDEFLVLALAHSLGSEMPAAMPGRCAAGVMHLFYVRAGVSRAMLRLFLAM 304

Qy 307 EKGHRMEYECPLYVVPVFAFRLEPKDGMFAVDGELMVSEAVQGGVHPNYFMVSGCV 366
Db 305 QKGHMLDCPLYVHPVFAFRLEPKDGMFAVDGELMVSEAVQGGVHPNYFMVSGCV 364

Qy 367 EPPSWKQPPPPPEEP 383
Db 365 DAPSGRDSRRGPPPPPEEP 381

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RESULT 12

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US-09-796-487-5
; Sequence 5, Application US/09796487
; Patent No. 6830916
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(373)
; OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHK1a in Fig. 2, co
; OTHER INFORMATION: rresponding to amino acid residue 131 to 504 of SPHK1a of GenBank
; OTHER INFORMATION: sequence Accession Number AAC61697.
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC61697
; DATABASE ENTRY DATE: 1998-09-26
; RELEVANT RESIDUES: (132)..(504)
US-09-796-487-5

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Query Match      79.6%; Score 1606.5; DB 4; Length 373;
Best Local Similarity 81.0%; Pred. No. 1.2e-172;
Matches 303; Conservative 34; Mismatches 36; Indels 1; Gaps 1;

Qy 10 VLPRPCRVLLVLPNGGKGKALQLFRSHVQPLLAAEABISFTMLTERNNHARELVRS 69
Db 1 LLRPPRCRVLLVLPNGGKGKALQLFQSRVQPFLEAEITFKLILTERKNHARELVCA 60

Qy 70 GRWDALVVMGSGDGLMHVVGNGLMERPDPWETAIOKPLCSLPAGSGNALAASLNHYAGYEQV 129
Db 61 GHWDAVVMGSGDGLMHVVGNGLMERPDPWETAIOKPLCSLPAGSGNALAASLNHYAGYEQV 120

Qy 130 TNEDLLTCTLLCRRLLSPMNLISHTASGLRFLSVLSLAWGFIADVDLSEKYYRRLGE 189
Db 121 TNEDLLTCTLLCRRLLSPMNLISHTASGLRFLSVLSLAWGFIADVDLSEKYYRRLGE 180

Qy 190 MRFTLGTFLRLAALRTYGRILAYLPVGRVSKTPASPVVQGGPVDLHLPLEPVP 249
Db 181 IRFTVGTFFRLASRLIYQGLAYLPVGTVAKRPPAS-TLVQKGPVDTHLVPLEPVP 239

Qy 250 TVVPDDEFLVLALAHSLGSEMPAAMPGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKG 309
Db 240 TVVPDQDFLLVLVLLHLSSELFAAMPGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKG 299

Qy 310 RHMEYECPLYVVPVFAFRLEPKDGMFAVDGELMVSEAVQGGVHPNYFMVSGCVPEPP 369
Db 300 KHMELDCPLYVHPVFAFRLEPKDGMFAVDGELMVSEAVQGGVHPNYFMVSGCVSDAP 359

Qy 370 PSWKQPPPPPEEP 383
Db 360 SGDRSRGPPPPPEEP 373

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RESULT 13

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US-09-205-258-328
; Sequence 328, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258

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Query Match      46.4%; Score 935.5; DB 4; Length 204;
Best Local Similarity 58.1%; Pred. No. 3.2e-97;
Matches 198; Conservative 4; Mismatches 2; Indels 137; Gaps 2;

QY 21 LNPRGGKALQFRSHVQPLLAEEAIEISFTLMLTERRNHARELVSEELGRWDALVVMVG 80
Db 1 LNPRGGKALQFRSHVQPLLAEEAIEISFTLMLTERRNHARELVSEELGRWDALVVMVG 60
QY 81 DGLMEHVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTL 140
Db 61 DGLMEHVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTL 107
QY 141 LLCRRLLSPMNLISHTASGLLFSVLSLANGFIADVDLESEKYRRLGEMRFTLTFLRL 200
Db 108 -----LFSVLSLANGFIADVDLESEKYRRLGEMRFTLTFLRL 145
QY 201 AALRTYRGLAYLPVGRVSKTPASPVVVQQGPVDHLVPLEEPVPSHWTVPDDEFLV 260
Db 146 AALRTYRGLATLPVGRVSK----- 166
QY 261 LALLSHLHSGEMFAAPMGRCAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYECPLYV 320
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RESULT 15
US-09-817-676A-12
; Sequence 12, Application US/09817676A
; Patent No. 6800470
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Kohama, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; FILE OF INVENTION: Expression and Methods of Use Thereof
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/194,318
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-817-676A-12

Query Match      44.3%; Score 894; DB 4; Length 617;
Best Local Similarity 39.9%; Pred. No. 8.9e-92;
Matches 192; Conservative 61; Mismatches 108; Indels 120; Gaps 5;

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Search completed: June 15, 2005, 12:12:13
Job time : 45 secs

GenCore version 5.1.6
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Run on: June 17, 2005, 02:31:28 ; Search time 5404 Seconds
(without alignments)
10804.688 Million cell updates/sec

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Perfect score: 1205
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb.ba.*
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- 3: gb.in.*
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- 9: gb.pr.*
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- 11: gb.sts.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1168.6	97.0	1821	6	BD157644 Primer fo
8	1168.6	97.0	1821	6	AX879091 Sequence
9	1168.6	97.0	1821	9	BC022402 Homo sapi
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14	1165.4	96.7	1815	9	BC008040 Homo sapi
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17	1162.6	96.5	1783	9	AF238083 Homo sapi
18	1149.4	95.4	1533	6	BD192995 207 human
19	1149.4	95.4	1533	6	CQ821991 Sequence

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ALIGNMENTS

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DEFINITION Sphingosine kinase.
ACCESSION BD267580
VERSION BD267580.1 GI:33077348
KEYWORDS JP 2002543831-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1205)
AUTHORS Pitson,S.M., Wattenberg,B.W., Xia,P., DGandrea,R.J., Gamble,J.R. and Vadas,M.A.
TITLE Sphingosine kinase
JOURNAL Patent: JP 2002543831-A 1 24-DEC-2002;
JOHNSON AND JOHNSON RESEARCH PTY LTD
COMMENT OS Mammalian
PN JP 2002543831-A/1
PD 24-DEC-2002
PF 12-MAY-2000 JP 2000618434
PR 13-MAY-1999 AU PQ 0339,08-JUL-1999 AU PQ 1504 PI
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PI JENNIFER RUTH GAMBLE,MATHEW ALEXANDER VADAS
PC C12N15/09,A61K31/711,A61K38/43,A61K38/55,A61K39/395,A61K39/395, PC
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AUTHORS	Pitson, S.M., Wattenberg, B.W., Xia, P., D'Andrea, R.J., Gamble, J.R. and Vadas, M.A.																											
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ACCESSION AX127641
VERSION AX127641.1 GI:14134307
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Allen J., Gosink M., Melendez, A.J. and Takacs, L.
TITLE Human sphingosine kinase gene
JOURNAL Patent: WO 0131029-A 1 03-MAY-2001;
WARNER-LAMBERT COMPANY (US)
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Db 1384 GGAAGCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGACC 1426

RESULT 7
BD157644
LOCUS BD157644 1821 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157644
VERSION BD157644.1 GI:27863402
KEYWORDS JP 2002191363-A/12487.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1821)
AUTHORS Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 12487 09-JUL-2002;
COMMENT
OS Homo sapiens (human)
PN JP 2002191363-A/12487
PD 09-JUL-2002

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Db 967 TCACCTCGGGCACTTTCCTGCTGTGGAGCTTGGGACCTTTCGGGACCTTACCGCGGCGCATGGCTT 1026

QY 667 ACCTCCCTGTAGGAGAGTGGTTCACAGACACCTGCTCCCGTGTGTGTGTCAGCTGGCGCTGG 726

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QY 1147 GGAAGCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1189

Db 1507 GGAAGCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGACC 1549

RESULT 9

AK022402 1821 bp mRNA linear PRI 30-JAN-2004

LOCUS Homo sapiens cDNA FLJ12340 fis, clone MAMMA1002268, moderately similar to Mus musculus sphingosine kinase (SPHK1a) mRNA.

DEFINITION AK022402

ACCESSION AK022402.1 GI:10433790

VERSION

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamiyama,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Hirakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Muraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togliya,S., Komai,F., Hara,R., Kato,K., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukushima,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Masuho,Y., Yamashita,R., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBMED 14702039

REFERENCE 2

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1821)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel.-81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES
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ORIGIN

Query Match 97.0%; Score 1168.6; DB 9; Length 1821;
 Best Local Similarity 99.2%; Pred. No. 6.8e-211; Mismatches 9; Indels 0; Gaps 0;
 Matches 1174; Conservative 0;

QY 7 GGCACGAGGAGCGCGGTCGAGGTATATGATCCAGCGGCGGCGCCCGCGGCGCGCTCC 66
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RESULT 10

BC030553
 LOCUS BC030553
 DEFINITION Homo sapiens sphingosine kinase 1, mRNA (cDNA clone MGC:40267
 IMAGE:5213270), complete cds.
 ACCESSION BC030553
 VERSION BC030553.1 GI:22539642
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2174)
 AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettner M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2174)

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	Db	324	GGCAGCGGAGCGCGGTCAGAGTTATGGATCCAGCGGGCGGCCCCCGGGCGTGCCTCC 383
	QY	67	CGCGGCCCTGCGCGTGTGTGCTGAACCCCGCGCGGGCGGCAAGGCGCAAGGCTTTCG 126
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	QY	127	AGCTCTTCGGAGTACAGTCGAGCCCTTTTGGCTGAGGCTGAATCTCCTTCACGCTGA 186
	Db	444	AGCTCTTCGGAGTACAGTCGAGCCCTTTTGGCTGAGGCTGAATCTCCTTCACGCTGA 503
	QY	187	TGCTCACTGAGCGCGGAACACGCGCGGAGCTGTGCGGTGCGAGGAGCTGGGCGGCT 246
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	QY	247	GGGACGCTCTGGTGGTCAATGCTCTGGAGACGGGCTGATGCACGAGTGTGTGAACGGGCTCA 306
Db	564	GGGACGCTCTGGTGGTCAATGCTCTGGAGACGGGCTGATGCACGAGTGTGTGAACGGGCTCA 623	
QY	307	TGGAGCGGCTGACTGGGAGACCGCCATCCAGAAGCCCTCTGTAGCCTCCAGCAGGCT 366	
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QY	367	CTGGCAACGCGCTGGCAGCTCTCTTGAACCAATTATGCTGGCTATGAGCAGGTTCACCAATG 426	
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QY	667	ACCTCCCTGTAGGAAGAGTGGGTTCACAGACACCTGCGCTCCCCCGTTGTGTCTCAGCAGG 726	
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Complete sequencing and characterization of 21,243 full-length			

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QY	1147	GGAAAGCCCCAGCAGATGCCACCGCCAGAGGCCCTTATGATC 1189
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RESULT 13		
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LOCUS Homo sapiens cDNA FLJ13331 fis, clone OVARC1001809, moderately		
DEFINITION similar to Mus musculus sphingosine kinase (SPHK1a) mRNA.		
ACCESSION AK023393		
VERSION AK023393.1 GI:10435311		
KEYWORDS oligo capping; fis (full insert sequence).		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Ishibashi, T., Yamashita, H., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, K., Kugahiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuko, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.		

REFERENCE AUTHORS	1 (bases 1 to 1815) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL MEDLINE PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257 12477932
REFERENCE AUTHORS	2 (bases 1 to 1815) Strausberg,R.
TITLE JOURNAL	Direct Submission Submitted (21-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov On Aug 19, 2003 this sequence version replaced gi:14165485. Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: ATCC/DC/DT/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbio.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
FEATURES source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row: n Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361087. Location/Qualifiers 1..1815 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:15041 IMAGE:3831657" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH_MGC_20" /lab_host="DH10B-R" /note="Vector: pOTB7" 1..1815 /gene="SPHK1" /note="synonym: SPHK" /db_xref="LocusID:8877" 330..1484 /db_xref="MIM:603730" /gene="SPHK1" /codon_start=1 /product="SPHK1 protein" /protein_id="AAH08040.1" /db_xref="GI:14165486" /db_xref="LocusID:8877" /db_xref="MIM:603730" /translation="MDPAGGPRGVLPRPRVLVLLNPRGGKALQLFRSHVQPLLA
gene	
CDS	

Db	907		GGGACGCTCTGTGTGTCATGCTGGAGACGGGCTGATGCACGAGGTGTGAACGGGCTCA	966
QY	307		TGGAGCGGCTGACTGGGAGACGGCCATCCAGAAGCCCTGTGTAGCTTCCAGCAGGCT	366
Db	967		TGGAGCGGCTGACTGGGAGACGGCCATCCAGAAGCCCTGTGTAGCTTCCAGCAGGCT	1026
QY	367		CTGGCAAGCGGCTGGCAGCTTCTTGAACCATATGCTGGCTATGAGCAGGTCAACCAATG	426
Db	1027		CTGGCAAGCGGCTGGCAGCTTCTTGAACCATATGCTGGCTATGAGCAGGTCAACCAATG	1086
QY	427		AAGACCTCTGACCAACTGACGCTATTGCTGTGCGCGGCTGCTGTCACCATGAACC	486
Db	1087		AAGACCTCTGACCAACTGACGCTATTGCTGTGCGCGGCTGCTGTCACCATGAACC	1146
QY	487		TGCTGTCTGTGCACACGGCTTCGGGCTGCGGCTTCTCTGTGTCTAGCCTGGCCTGGG	546
Db	1147		TGCTGTCTGTGCACACGGCTTCGGGCTGCGGCTTCTCTGTGTCTAGCCTGGCCTGGG	1206
QY	547		GCTTCATTGCTGATGTGACCTAGAGAGTGAGAGATTCGGGCTTCGGGGAGATGCCCT	606
Db	1207		GCTTCATTGCTGATGTGACCTAGAGAGTGAGAGATTCGGGCTTCGGGGAGATGCCCT	1266
QY	607		TCACCTCTGGGCACTTTCCTGTGCTGTGGCAGCCTTGCGCACTTACCGCGGCGACTGGGCTT	666
Db	1267		TCACCTCTGGGCACTTTCCTGTGCTGTGGCAGCCTTGCGCACTTACCGCGGCGACTGGGCTT	1326
QY	667		ACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCTCCCGTTGTGTGTCCAGCAGG	726
Db	1327		ACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCTCCCGTTGTGTGTCCAGCAGG	1386
QY	727		GCCCGGTAGATGCACACCTTGTGCCACTGGAAGGACGAGTGCCCTCTCACTGGACAGTGG	786
Db	1387		GCCCGGTAGATGCACACCTTGTGCCACTGGAAGGACGAGTGCCCTCTCACTGGACAGTGG	1446
QY	787		TGCCCGAGAGGACTTGTGTAGTCTGTGGCACTGCTGCACCTCGCACCTGGGCGAGTGAGA	846
Db	1447		TGCCCGAGAGGACTTGTGTAGTCTGTGGCACTGCTGCACCTCGCACCTGGGCGAGTGAGA	1506
QY	847		TGTTTGTCTGCAACCCATGGGCGGCTGTGCAGCTGGCGTCAATGCATCTGTTTACGTGGGG	906
Db	1507		TGTTTGTCTGCAACCCATGGGCGGCTGTGCAGCTGGCGTCAATGCATCTGTTTACGTGGGG	1566
QY	907		CGGGAGTCTCTGTGCGATGCTGCGGCTTCTTCTGGCCATGGAGAGGGGCGAGGCATA	966
Db	1567		CGGGAGTCTCTGTGCGCATGCTGCGGCTTCTTCTGGCCATGGAGAGGGGCGAGGCATA	1626
QY	967		TGGAGTATGAATGCCCTTACTTGGTATATGTGCCCGTGGTGGCTTCCGCTTGGAGCCCA	1026
Db	1627		TGGAGTATGAATGCCCTTACTTGGTATATGTGGTATACGTGCCGTGGTGGCTTCCGTTGGAGCCCA	1686
QY	1027		AGGATGGGAAGGTTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCAGGCCGTGCAGG	1086
Db	1687		AGGATGGGAAGGTTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCAGGCCGTGCAGG	1746
QY	1087		GCCAGGTGCACCCAACTACTTCTGGATGCTCAGGGTTGCGTGGAGCCCCCGGCCAGCT	1146
Db	1747		GCCAGGTGCACCCAACTACTTCTGGATGCTCAGGGTTGCGTGGAGCCCCCGGCCAGCT	1806
QY	1147		GGAGCCCCCAGCAGATGCCACCGCCAGAAAGCCCTTATGATC	1189
Db	1807		GGAGCCCCCAGCAGATGCCACCGCCAGAAAGCCCTTATGACC	1849

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 02:28:43 ; Search time 728 Seconds
(without alignments)
9798.473 Million cell updates/sec

Title: US-10-642-289-1
Perfect score: 1205
Sequence: 1 gaattcgagcagagcg.....gatctagatgcacctgcag 1205

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1205	100.0	1205	5 AAC84161	Aac84161 Human sph
2	1173	97.3	1173	6 ABL59532	Ab159532 Human sph
3	1168.6	97.0	1573	3 AAA75676	Aaa75676 DNA encod
4	1168.6	97.0	1719	5 AAD04477	Aad04477 Human sph
5	1168.6	97.0	1821	4 AAH15652	Aah15652 Human cdn
6	1168.6	97.0	2137	10 ADD29776	Add29776 Human tum
7	1168.2	96.9	1799	10 ADE38364	Ade38364 Human pro
8	1167	96.8	1772	4 AAH16415	Aah16415 Human cdn
9	1162.6	96.5	1783	12 ADQ17904	Adq17904 Human sof
10	1149.4	95.4	1533	2 AAV84490	Aav84490 Human sec
11	1149.4	95.4	1533	4 ABA83273	Aba83273 Human sec
12	1149.4	95.4	1533	9 ACH04774	Ach04774 Novel hum
13	1149.4	95.4	1533	9 ACD44584	Acd44584 Human cdn
14	1147	95.2	1155	6 ABK90198	Abk90198 CDNA enco
15	1145.8	95.1	1438	4 AAI59336	Aai59336 Human pol
16	1143.8	94.9	1447	3 AAA50508	Aaa50508 Human sph
17	1142.4	94.8	1152	9 ACF35857	Acf35857 Human sph
18	1141.4	94.7	1600	5 AAD14424	Aad14424 Human sph
19	1140.4	94.6	1562	6 ABL90618	Ab190618 Human pol
20	1140.4	94.6	1869	12 ADJ74940	Adj74940 Marker ge

21	1140.4	94.6	1869	12 ADO22416	Ado22416 Human sph
22	1140	94.6	1197	12 ADO22418	Ado22418 Human sph
23	1115.2	92.5	2551	12 ADO22519	Ado22519 Human sof
24	910.8	75.6	1200	4 AAI61122	Aai61122 Human pol
25	770.4	63.9	1759	5 AAD14425	Aad14425 Mouse con
26	760	63.1	1149	6 ABK90200	Abk90200 CDNA enco
27	757.6	62.9	1815	3 AAZ47167	Aaz47167 Mouse sph
28	756.6	62.8	1559	3 AAZ47168	Aaz47168 Mouse sph
29	756.6	62.8	1559	12 ADJ75835	Adj75835 Marker ge
30	752	62.4	1146	10 ABZ81300	Abz81300 Mouse sph
31	272	22.6	675	4 AAH07214	Aah07214 Human cdn
32	258	21.4	1857	6 ABK90199	Abk90199 CDNA enco
33	258	21.4	2380	5 AAS14817	Aas14817 Human cdn
34	258	21.4	2380	5 ABL59533	Ab159533 Human sph
35	258	21.4	2380	10 ADE85298	Ade85298 Farnesyl
36	258	21.4	2380	10 ADE38416	Ade38416 Human pro
37	258	21.4	2380	12 ADQ5181	Adq15181 Human can
38	258	21.4	2422	5 AAS85331	Aas85331 DNA encod
39	258	21.4	2682	13 ADQ83707	Adq83707 Human tum
40	258	21.4	2682	13 ADQ87011	Adq87011 Human tum
41	258	21.4	2875	5 ABX71285	Abx71285 Human sig
42	245.2	20.3	2698	5 AAS14816	Aas14816 Mouse cdn
43	240	19.9	240	5 AAD04478	Aad04478 Conserved
44	235	19.5	587	4 AAH10443	Aah10443 Human cdn
45	227.8	18.9	549	13 ADQ49460	Adq49460 Novel can

ALIGNMENTS

RESULT 1
AAC84161
ID AAC84161 standard; CDNA; 1205 BP.
AC AAC84161;
DT 19-MAR-2001 (first entry)
DE Human sphingosine kinase encoding CDNA.
XX Sphingosine kinase; antiarthritic; antiaethmatic; antiarteriosclerotic;
KW antinflammatory; neuroprotective; antibacterial; immunosuppressive;
KW human; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 33..1187
FT /*tag= a
FT /product= "sphingosine kinase"
XX
PN WO200070028-A1.
XX
XX 23-NOV-2000.
XX 12-MAY-2000; 2000WO-AU000457.
XX 13-MAY-1999; 99AU-00000339.
PR 08-JUL-1999; 99AU-00001504.
XX
XX (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
XX Pitson SM, Wattenberg BW, Xia P, D'andrea RJ, Gamble JR;
PI Vadas MA;
XX
XX WPI; 2001-016227/02.
XX P-PSDB; AAB48007.
XX
XX Novel sphingosine kinase protein and nucleic acid molecules for
XX diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma,
XX atherosclerosis, inflammation, meningitis, multiple sclerosis and septic
XX shock.

PS Claim 4; Fig 7a; 100pp; English.

XX This cDNA encodes a human sphingosine kinase (SK) protein. The human SK protein, encoding nucleic acids and modulators are useful for modulating expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by modulating the activity of SK. Diseases treated by regulating SK cellular activity include rheumatoid arthritis, asthma, atherosclerosis, CC inflammation, meningitis, multiple sclerosis and septic shock

XX Sequence 1205 BP; 196 A; 357 C; 400 G; 252 T; 0 U; 0 Other;

Query Match 100.0%; Score 1205; DB 5; Length 1205;
Best Local Similarity 100.0%; Pred. No. 2.1e-266;
Matches 1205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTTCGGACACGAGGACCGCGGTCGAGGTATGATTCACGCGCGCGCCCGCGGCG 60

DB 1 GAATTTCGGACACGAGGACCGCGGTCGAGGTATGATTCACGCGCGCGCCCGCGGCG 60

QY 61 TGCCTCCGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

DB 61 TGCCTCCGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 CCTTCAGCTCTTCGGAGTCAGTCAGCCCTTTTGGCTGAGGCTGAATCTCTTCA 180

DB 121 CCTTCAGCTCTTCGGAGTCAGTCAGCCCTTTTGGCTGAGGCTGAATCTCTTCA 180

QY 181 CGCTGATGCTCACTGAGCGCGGGAACACCGCGCGGAGCTGGTGGCTGGAGGAGCTGG 240

DB 181 CGCTGATGCTCACTGAGCGCGGGAACACCGCGCGGAGCTGGTGGCTGGAGGAGCTGG 240

QY 241 GCCGTGGGACCGCTCTGGTGTCTGTCATGTCGAGACCGGCTGATGACAGGCTGGTGAACG 300

DB 241 GCCGTGGGACCGCTCTGGTGTCTGTCATGTCGAGACCGGCTGATGACAGGCTGGTGAACG 300

QY 301 GGTCTATGAGCGGCTGACTGGGAGACCGCATCCAGAGCCCTGTGTAGCTCCCGAG 360

DB 301 GGTCTATGAGCGGCTGACTGGGAGACCGCATCCAGAGCCCTGTGTAGCTCCCGAG 360

QY 361 CAGGCTCTGGCAACCGCTGGCAGCTTCTTGAACCATTTATGCTGGCTATGAGCAGGTCA 420

DB 361 CAGGCTCTGGCAACCGCTGGCAGCTTCTTGAACCATTTATGCTGGCTATGAGCAGGTCA 420

QY 421 CCAATGAAGACCTCTGACCACTGACGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

DB 421 CCAATGAAGACCTCTGACCACTGACGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY 481 TGAACCTGCTGCTCTGCACACGGCTTCGGGCTGCGCTCTTCTGCTGCTGCTGCTGCTGCTG 540

DB 481 TGAACCTGCTGCTCTGCACACGGCTTCGGGCTGCGCTCTTCTGCTGCTGCTGCTGCTGCTG 540

QY 541 CTTGGGGCTTCAATGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCTCTGGGGGAGA 600

DB 541 CTTGGGGCTTCAATGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCTCTGGGGGAGA 600

QY 601 TGGCTTCACTCTGGGACCTTTCTGCGTCTGGGAGCCTTGGGACCTTACCGCGCGCCGAC 660

DB 601 TGGCTTCACTCTGGGACCTTTCTGCGTCTGGGAGCCTTGGGACCTTACCGCGCGCCGAC 660

QY 661 TGGCTTACCTCCCTGTAGGAGAGTGGTTCAGACACCTGCTCCCGCTGGTGGTCC 720

DB 661 TGGCTTACCTCCCTGTAGGAGAGTGGTTCAGACACCTGCTCCCGCTGGTGGTCC 720

QY 721 AGCAGGGCCGGTAGATGACACCTTGTGCCACTGGAGGACGAGTGGCCCTCTCACTGGA 780

DB 721 AGCAGGGCCGGTAGATGACACCTTGTGCCACTGGAGGACGAGTGGCCCTCTCACTGGA 780

QY 781 CAGTGGTCCGACGAGGACCTTTGTGCTAGTCTGGGACCTGCTGACCTCGACCTGGGCA 840

DB 781 CAGTGGTCCGACGAGGACCTTTGTGCTAGTCTGGGACCTGCTGACCTCGACCTGGGCA 840

QY 841 GTGAGATGTTTGTGCACCCATGGGCGCTGTGAGCTGGCGTCAATGCTGTTCTTACG 900

DB 841 GTGAGATGTTTGTGCACCCATGGCGCTGTGAGCTGGCGTCAATGCTGTTCTACG 900

QY 901 TCGGGCGGGAGTGTCTCGTGCCATGCTGCTGCGCCTTCTCTGCGCCATGGAGAAGGCA 960

DB 901 TCGGGCGGGAGTGTCTCGTGCCATGCTGCTGCGCCTTCTCTGCGCCATGGAGAAGGCA 960

QY 961 GGCATATGGAGTATGAATGCCCTTACTTGGTATATGTGCCGCTGCTGCGCTTCCGCTTGG 1020

DB 961 GGCATATGGAGTATGAATGCCCTTACTTGGTATATGTGCCGCTGCTGCGCTTCCGCTTGG 1020

QY 1021 AGCCCAAGGATGGAAAGGTATGTTTGCAGTGAATGGGAATTCATGCTAGCGAGGCGG 1080

DB 1021 AGCCCAAGGATGGAAAGGTATGTTTGCAGTGAATGGGAATTCATGCTAGCGAGGCGG 1080

QY 1081 TSCAGGGCCAGGTGCACCCAACTACTTCTGGATGGTCAGCGGTTCGCTGGAGCCCCCGC 1140

DB 1081 TSCAGGGCCAGGTGCACCCAACTACTTCTGGATGGTCAGCGGTTCGCTGGAGCCCCCGC 1140

QY 1141 CCAGCTGGAGCCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATCTAGAGTCGACC 1200

DB 1141 CCAGCTGGAGCCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATCTAGAGTCGACC 1200

QY 1201 TGCAG 1205

DB 1201 TGCAG 1205

RESULT 2

ABL59532

ID ABL59532 standard; cDNA; 1173 BP.

XX

AC ABL59532;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human sphingosine kinase (SphK1) cDNA SEQ ID NO:32.

XX

XX Human; sphingosine kinase; SphK1; enzyme; chromosome 17q25.2; gene; tumour; lipid associated gene; lipid metabolism; lipid synthesis; ss.

KW

XX Homo sapiens.

OS

XX WO200227028-A1.

PN

XX

PD 04-APR-2002.

PF

XX 27-SEP-2001; 2001WO-US030366.

PR

XX 28-SEP-2000; 2000US-00676052.

XX

PA (ATAI-) APAIRGIN TECHNOLOGIES INC.

XX

XX Skinner MK, Patton JL, Chaudhary J;

XX

XX WPI; 2002-405056/43.

DR

XX

PT Identifying tumor characteristics in a tissue sample taken from a patient, involves determining the copy number or expression level of genes associated with lipid metabolism, synthesis or action.

PT

XX

PS Example 1; Page 90; 113pp; English.

XX

CC The present invention describes a method for identifying tumour characteristics, comprising measuring a copy number or expression level of at least two genes associated with lipid metabolism, synthesis, or action in cells from a patient tissue sample, and comparing the results with a copy number or expression level of the genes in a normal cell.

CC

CC Also described is an array of nucleic acid polymers immobilised on a solid support, comprising a solid support, at least two different nucleic acid polymers which are each specific for a different gene associated with lipid metabolism, synthesis or action, where each nucleic acid polymer is located at a predetermined position on the solid support, and

CC antagonists of HRP polypeptide. HRP and its agonist or antagonist are
CC useful for treating a disease or condition associated with decreased or
CC increased expression of functional HRP. Diseases treated or diagnosed
CC include neurological disorders such as stroke, Parkinson's disease,
CC demyelinating diseases, bacterial and viral meningitis and other
CC developmental disorders of the central nervous system, neuromuscular
CC disorders, myasthenia gravis, cell proliferative disorders such as
CC actinic keratosis, arteriosclerosis, atherosclerosis and cancer including
CC leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder,
CC bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory
CC disorder such as Addison's disease, acquired immunodeficiency diseases,
CC allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial
CC infection and trauma

XX Sequence 1573 BP; 274 A; 480 C; 514 G; 305 T; 0 U; 0 Other;

Query Match 97.0%; Score 1168.6; DB 3; Length 1573;
Best Local Similarity 99.2%; Pred. No. 4.9e-258;
Matches 1174; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 7 GGCACAGAGCGCGGCTCGAGGTATGGATCCAGCGGCGGCGCGCGGCGGTGCTCC 66
DB 104 GCGCGGAGCGCGGCTCGAGGTATGGATCCAGCGGCGGCGCGCGGCGGTGCTCC 163
QY 67 CGCGGCGCTGCGGCTGCTGCTGCTGAACCCGCGGCGGCGGCGGCGGCGGCTTGC 126
DB 164 CGCGGCGCTGCGGCTGCTGCTGCTGAACCCGCGGCGGCGGCGGCGGCGGCTTGC 223
QY 127 AGCTCTTCGCGAGTCACGTGCGAGCCCTTTTGGCTGAGGCTGAAATCTCTTCACGCTGA 186
DB 224 AGCTCTTCGCGAGTCACGTGCGAGCCCTTTTGGCTGAGGCTGAAATCTCTTCACGCTGA 283
QY 187 TGCTCACTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 246
DB 284 TGCTCACTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 343
QY 247 GGGAGCTCTGCTGCTCATGCTCGGAGCGGCTCATGCGAGGCTGCTGAGCGGCTCA 306
DB 344 GGGAGCTCTGCTGCTCATGCTCGGAGCGGCTCATGCGAGGCTGCTGAGCGGCTCA 403
QY 307 TGGAGCGGCTGACTGGGAGACCGCATCCAGAACCCCTGTGTAGCTCCCGAGCGCT 366
DB 404 TGGAGCGGCTGACTGGGAGACCGCATCCAGAACCCCTGTGTAGCTCCCGAGCGCT 463
QY 367 CTGGCAACGCTGCGAGCTTCTTGACCATATGCTGGCTATGAGAGGCTCAACATG 426
DB 464 CTGGCAACGCTGCGAGCTTCTTGACCATATGCTGGCTATGAGAGGCTCAACATG 523
QY 427 AAGACCTCTGACCACTGACGCTATTGCTGCGCGGCTGCTGTCACCATGAACC 486
DB 524 AAGACCTCTGACCACTGACGCTATTGCTGCGCGGCTGCTGTCACCATGAACC 583
QY 487 TGCTGCTCTGCACACGCTTCGGGCTCGGCTCTTCTGTGTCTGAGCTTGGCTGG 546
DB 584 TGCTGCTCTGCACACGCTTCGGGCTCGGCTCTTCTGTGTCTGAGCTTGGCTGG 643
QY 547 GCTTCATTGCTGATGTGACCTAGAGAGTGAAGATATCGGCTCTGGGGAGATGCGCT 606
DB 644 GCTTCATTGCTGATGTGACCTAGAGAGTGAAGATATCGGCTCTGGGGAGATGCGCT 703
QY 607 TCACCTCTGGGCACTTCTGCTGCTGCGGAGCTTACCGGCTTACCGGCGGAGCTGGGTT 666
DB 704 TCACCTCTGGGCACTTCTGCTGCTGCGGAGCTTACCGGCTTACCGGCGGAGCTGGGTT 763
QY 667 ACCTCCCTGTAGGAAGTGGGTTCCAGACACCTGCTCCCGTGTGTGCTCCAGCAGG 726
DB 764 ACCTCCCTGTAGGAAGTGGGTTCCAGACACCTGCTCCCGTGTGTGCTCCAGCAGG 823
QY 727 GCGCGGTAGATGCACACCTTGTGCTGCTGAGGAGCGGCTTCTCACTGGACAGTGG 786
DB 824 GCGCGGTAGATGCACACCTTGTGCTGCTGAGGAGCGGCTTCTCACTGGACAGTGG 883
QY 787 TGCCCGGACGAGGACTTTGTGCTAGTCTGCGCACTGCTGCACTCGCACCTGGGCGAGTGA 846

DB 884 TGCCCGACGAGACTTGTGTAGTCTCTGGCACTGCTGCACCTGGGCACTGAGA 943
QY 847 TGTTCGTGACCATGGCGCTGTGAGCTGCGCTCATGCTATGTTCTACGTGGGG 906
DB 944 TGTTCGTGACCATGGCGCTGTGAGCTGCGCTCATGCTATGTTCTACGTGGGG 1003
QY 907 CGGAGTGTCTCGTCCCATGCTGCTGCGCTTCTTCTGGCCATGGAGGCGGAGCATA 966
DB 1004 CGGAGTGTCTCGTCCCATGCTGCTGCGCTTCTTCTGGCCATGGAGGCGGAGCATA 1063
QY 967 TGGAGTATGAATGCGCTTACTTGTATATGTCGCGCTTCCGCTTGGAGGCCA 1026
DB 1064 TGGAGTATGAATGCGCTTACTTGTATATGTCGCGCTTCCGCTTGGAGGCCA 1123
QY 1027 AGGATGGAAAGGTATGTTTGCAGTGGATGGGAAATGATGTTAGGAGCCCTGTCAGG 1086
DB 1124 AGGATGGAAAGGTGTGTTTGCAGTGGATGGGAAATGATGTTAGGAGCCCTGTCAGG 1183
QY 1087 GCCAGGTGACCCCAACTACTTCTGGATGCTCAGGCTTGGTGAGCCCGGCCAGCT 1146
DB 1184 GCCAGGTGACCCCAACTACTTCTGGATGCTCAGGCTTGGTGAGCCCGGCCAGCT 1243
QY 1147 GGAAGCCCCAGCAGATGCCCGCCAGAGAGCCCTTATGATC 1189
DB 1244 GGAAGCCCCAGCAGATGCCCGCCAGAGAGCCCTTATGACC 1286
RESULT 4
AAD04477
ID AAD04477 standard; cDNA; 1719 BP.
XX AAD04477;
DT 04-JUL-2001 (first entry)
XX Human sphingosine kinase type 1 (hsk1) cDNA.
DE Human; sphingosine kinase type 1; skl; chromosome 17q25.2;
KW sphingosine-1-phosphate; SIP; drug screening; therapy; haemostasis;
KW thrombosis; allergic reaction; proliferative disease; cancer;
KW haematopoietic disorder; leukaemia; cardiovascular disease; stroke;
KW atherosclerosis; coronary artery disease; dyslipidaemia; diabetes;
KW autoimmune disease; inflammatory disease; multiple sclerosis;
KW T helper-1 related disease; chronic obstructive pulmonary disease;
KW asthma; myocardial infarction; neurodegenerative disorder; wound healing;
KW embryogenesis; anticoagulant; cerebroprotective; neuroprotective;
KW antipsoriatic; antiarthritic; cytostatic; cardiant; vulnerary; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature /*tag= C
FT /*note= "Translational initiator ATG is in a partial Kozak
FT consensus"
FT CDS 270..1424
FT /*tag= a
FT /*product= "Human sphingosine kinase type 1 (hsk1)"
FT /*note= "CDS is specifically claimed in claim 2 and shown
FT polyA_signal 1675..1681
FT /*tag= b
XX WO200131029-A2.
PN 03-MAY-2001.
PD 27-OCT-2000; 2000WO-EP009498.
PF 28-OCT-1999; 99US-0162307P.
PR 07-FEB-2000; 2000US-0180525P.
XX

(WARN) WARNER LAMBERT CO.
PA Allen J, Gosink M, Melendez AJ, Takacs L;
XX WPI; 2001-300510/31.
PI P-PSDB; AAE00924.
XX
DR New human sphingosine kinase type 1 gene for screening drug candidates
XX particularly inhibitors used for preventing or treating e.g.
PT atherosclerosis, thrombosis, asthma and diabetes.
PT
XX Claim 2; Fig 1; 91pp; English.
PS
XX The present sequence is human sphingosine kinase type 1 (hsk1) cDNA. The
CC hsk1 gene is located on chromosome 1q25.2. The sk1 converts the
CC substrate sphingosine to sphingosine-1-phosphate (S1P). The sk1 gene and
CC encoded polypeptide are applicable in screening drug candidates
CC particularly inhibitors for preventing or treating disorders such as
CC haemostasis, thrombosis, allergic reactions, proliferative diseases
CC including cancer, haematopoietic disorders such as leukaemia,
CC cardiovascular diseases such as stroke, atherosclerosis and coronary
CC artery disease, dyslipidaemia, diabetes including type I and type II
CC diabetes, autoimmune and inflammatory diseases such as multiple
CC sclerosis, T helper-1 related diseases, chronic obstructive pulmonary
CC disease, asthma, myocardial infarction, neurodegenerative disorders,
CC natural wound healing processes and embryogenesis.
XX
XX Sequence 1719 BP; 305 A; 529 C; 556 G; 329 T; 0 U; 0 Other;
Query Match 97.0%; Score 1168.6; DB 5; Length 1719;
Best Local Similarity 99.2%; Pred. No. 5e-258; 9; Indels 0; Gaps 0;
Matches 1174; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 7 GGCAACGAGGCGCGGGTCGAGGTTATGATATCCAGCGCGCGCGCGCGCGCGCTCC 66
DB 244 GGCAGCGGAGCGCGGGTCGAGGTTATGATATCCAGCGCGCGCGCGCGCGCTCC 303
QY 67 CGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
DB 304 CGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
QY 127 AGCTCTTCGCGAGTCAGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGA 186
DB 364 AGCTCTTCGCGAGTCAGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGA 423
QY 187 TGCTCACTGAGCGCGGAAACACGCGCGGAGCTGCTGCGGTCGAGGAGCTGGCGCGCT 246
DB 424 TGCTCACTGAGCGCGGAAACACGCGCGGAGCTGCTGCGGTCGAGGAGCTGGCGCGCT 483
QY 247 GGCACGCTTGGTGCTCATGCTGAGAGACGCGGCTGATGACGAGGCTGTAACGGGCTCA 306
DB 484 GGCACGCTTGGTGCTCATGCTGAGAGACGCGGCTGATGACGAGGCTGTAACGGGCTCA 543
QY 307 TGGAGCGGCTGAGCTGGAGACCGCCATCCAGAGCGCGCGCGCGCGCGCGCGCTGCT 366
DB 544 TGGAGCGGCTGAGCTGGAGACCGCCATCCAGAGCGCGCGCGCGCGCGCGCGCTGCT 603
QY 367 CTGGCAACCGCGCTGGAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCACCAATG 426
DB 604 CTGGCAACCGCGCTGGAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCACCAATG 663
QY 427 AAGACCTCTGACCAACTGACGCTATGCTGTCGCGCGCGCGCGCGCGCGCTGCTGACCCATGACC 486
DB 664 AAGACCTCTGACCAACTGACGCTATGCTGTCGCGCGCGCGCGCGCGCTGCTGACCCATGACC 723
QY 487 TGCTGCTCTGACACGCGCTTGGGGCTGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 546
DB 724 TGCTGCTCTGACACGCGCTTGGGGCTGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 783
QY 547 GCTTCATTGCTGATGTGGACCTAGAGAGTGAGAGTATCGCGCTGCTGGGGGAGATGCGCT 606
DB 784 GCTTCATTGCTGATGTGGACCTAGAGAGTGAGAGTATCGCGCTGCTGGGGGAGATGCGCT 843

QY 607 TCACTCTGGGCACTTTCTCGCTCTGGCAGCGCTTGGGCACTTACCGGGGCCGACTGGCTT 666
DB 844 TCACTCTGGGCACTTTCTCGCTCTGGCAGCGCTTGGGCACTTACCGGGGCCGACTGGCTT 903
QY 667 ACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGGTTGTGTGTGTGTGTGTGT 726
DB 904 ACCTCCCTGTAGGAAGAGTGGGTTCCAAAGACACCTGCTCCCGGTTGTGTGTGTGTGTGTGT 963
QY 727 GCCCGGTAGATGCACACCTTGTGCGACCTGGAGAGCCAGTGCCTCTCACTGGACAGTGG 786
DB 964 GCCCGGTAGATGCACACCTTGTGCGACCTGGAGAGCCAGTGCCTCTCACTGGACAGTGG 1023
QY 787 TGCCCGACAGGACTTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
DB 1024 TGCCCGACAGGACTTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
QY 847 TGTGTTGCTGACCCCATGCGGCGCTGTGCGAGCTGGGGTTCATGCTGTTCTACGTTGCGGG 906
DB 1084 TGTGTTGCTGACCCCATGCGGCGCTGTGCGAGCTGGGGTTCATGCTGTTCTACGTTGCGGG 1143
QY 907 CGGGAGTGTCTGCTGCCATGCTGCTGCGCCCTTCTTCTGCGCATGGAGAAGGCGAGGCATA 966
DB 1144 CGGGAGTGTCTGCTGCCATGCTGCTGCGCCCTTCTTCTGCGCATGGAGAAGGCGAGGCATA 1203
QY 967 TGGAGTATGAATGCCCCCTACTTGTGATATGTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
DB 1204 TGGAGTATGAATGCCCCCTACTTGTGATATGTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
QY 1027 AGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTCATGTTAGCGAGCGCGTGCAGG 1086
DB 1264 AGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTCATGTTAGCGAGCGCGTGCAGG 1323
QY 1087 GCCAGGTGCACCAACTACTTCTGATGTTGTCAGCGGTTGCGTGGAGCGCGCGCGCGCGCT 1146
DB 1324 GCCAGGTGCACCAACTACTTCTGATGTTGTCAGCGGTTGCGTGGAGCGCGCGCGCGCGCT 1383
QY 1147 GGAAGCGCGCAGAGATGCCACCGCCAGAGAGCCCTTATGATC 1189
DB 1384 GGAAGCGCGCAGAGATGCCACCGCCAGAGAGCCCTTATGATC 1426
RESULT 5
AAH15652
ID AAH15652 standard; cDNA; 1821 BP.
XX
AC AAH15652;
XX
XX 26-JUN-2001 (first entry)
XX Human cDNA sequence SEQ ID NO:13996.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000BP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
DR

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 8; SEQ ID NO 13996; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX Sequence 1821 BP; 301 A; 569 C; 614 G; 337 T; 0 U; 0 Other;

Query Match 97.0%; Score 1168.6; DB 4; Length 1821;
Best Local Similarity 99.2%; Pred. No. 5.1e-258;
Matches 1174; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 7 GCACGAGGAGCGCGGTGAGGTATGATCCAGCGGCGGCCCCCGGGCGTGTCC 66
DB |||||
QY 367 GCACGCGGAGCGCGGGTGCAGGTATGATCCAGCGGCGGCCCCCGGGCGTGTCC 426
DB |||||
QY 67 CGCGGCGCTGCGCGTGTGCTGCTGAACCCCGCGGCGGCAAGGCGCTTGC 126
DB |||||
QY 427 CGCGGCGCTGCGCGTGTGCTGCTGAACCCCGCGGCGGCAAGGCGCTTGC 486
DB |||||
QY 127 AGCTCTTCGGAGTCACTGTCAGCGCCCTTTTGGCTGAGGCTGAATCTCTTCA 186
DB |||||
QY 487 AGCTCTTCGGAGTCACTGTCAGCGCCCTTTTGGCTGAGGCTGAATCTCTTCA 546
DB |||||
QY 187 TGCTCACTGAGCGGCGGAACACGCGGCGGAGCTGGTGGCTCGGAGAGCTGGGCG 246
DB |||||
QY 547 TGCTCACTGAGCGGCGGAACACGCGGCGGAGCTGGTGGCTCGGAGAGCTGGGCG 606
DB |||||
QY 247 GGGAGCGCTCTGGTGTCTATGCTCGAGACGGGCTGATGCAGAGTGGTGAACGGGCTCA 306
DB |||||
QY 607 GGGAGCGCTCTGGTGTCTATGCTCGAGACGGGCTGATGCAGAGTGGTGAACGGGCTCA 666
DB |||||
QY 307 TGGAGCGGCGTGACTGGGAGACCGCCATCCAGAACGCCCTTGTAGCTTCCAGCAGCT 366
DB |||||
QY 667 TGGAGCGGCGTGACTGGGAGACCGCCATCCAGAACGCCCTTGTAGCTTCCAGCAGCT 726
DB |||||
QY 367 CTGGCAACGCGCTGCGAGCTCTTGAACCATATGCTGGCTATGAGCAGGTCAACCAATG 426
DB |||||
QY 727 CTGGCAACGCGCTGCGAGCTCTTGAACCATATGCTGGCTATGAGCAGGTCAACCAATG 786
DB |||||
QY 427 AAGACTCTCTGACCACTGACGCTATGCTGTGCGCGGCTGTGTCAACCATGAACC 486
DB |||||
QY 787 AAGACTCTCTGACCACTGACGCTATGCTGTGCGCGGCTGTGTCAACCATGAACC 846
DB |||||
QY 487 TGCTGTCTGTGCACACGGCTTCGGGCGTGGCGCTCTTCTGTGTGTCAAGCTTGGCTGGG 546
DB |||||
QY 847 TGCTGTCTGTGCACACGGCTTCGGGCGTGGCGCTCTTCTGTGTGTCAAGCTTGGGCTGGG 906
DB |||||

QY 547 GCTTCATTGCTGATGTGACCTAGAGAGTGAAGAGTATCGGCGTCTGGGGAGATGCGCT 606
DB |||||
QY 907 GCTTCATTGCTGATGTGACCTAGAGAGTGAAGAGTATCGGCGTCTGGGGAGATGCGCT 966
DB |||||
QY 607 TCACTCTGGGCACTTTCCTGCGTCTGCGAGCTTTGGCAGCTTACCGGGGCGGCACTGGGCTT 666
DB |||||
QY 967 TCACTCTGGGCACTTTCCTGCGTCTGCGAGCCCTTGGCAGCTTACCGGGGCGGCACTGGGCTT 1026
DB |||||
QY 667 ACCTCCCTGTAGGAAGAGTGGTTTCCAAAGACACCTGCTCTCCCGTGTGTGTGTCAGCAGG 726
DB |||||
QY 1027 ACCTCCCTGTAGGAAGAGTGGTTTCCAAAGACACCTGCTCTCCCGTGTGTGTGTCAGCAGG 1086
DB |||||
QY 727 GCCCGGTAGTAGCACACTTGTGCGCACTGGAGAGCCAGTGCCTCTCACTTGGACAGTGG 786
DB |||||
QY 1087 GCCCGGTAGTAGCACACTTGTGCGCACTGGAGAGCCAGTGCCTCTCACTTGGACAGTGG 1146
DB |||||
QY 787 TGCCCGCAGCAGGACTTTTGTGTAGTCTGTGCACTGTGCACTCGCACCTGGGCGAGTGAGA 846
DB |||||
QY 1147 TGCCCGCAGCAGGACTTTTGTGTAGTCTGTGCACTGTGCACTCGCACCTGGGCGAGTGAGA 1206
DB |||||
QY 847 TGTGTGTGCAACCATGCGCGCTGTGCACTGTGCGCTCATGCATCTGTTCACGTGCGGG 906
DB |||||
QY 1207 TGTGTGTGCAACCATGCGCGCTGTGCACTGTGCGCTCATGCATCTGTTCACGTGCGGG 1266
DB |||||
QY 907 CGGAGTGTCTCGTGCCATGCTGCTGCGCTTCTCTGGCCATGGAGAGGGGAGGCATATA 966
DB |||||
QY 1267 CGGAGTGTCTCGTGCCATGCTGCTGCGCTTCTCTGGCCATGGAGAGGGGAGGCATATA 1326
DB |||||
QY 967 TGGAGTATGAATGCGCCCTACTTGTGTATATGTGCGCGTGGTGGCTTCCGCTTGGAGGCCA 1026
DB |||||
QY 1327 TGGAGTATGAATGCGCCCTACTTGTGTATATGTGCGCGTGGTGGCTTCCGCTTGGAGGCCA 1386
DB |||||
QY 1027 AGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTTGATGGTTAGCGAGCCCGTGCAGG 1086
DB |||||
QY 1387 AGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTTGATGGTTAGCGAGCCCGTGCAGG 1446
DB |||||
QY 1087 GCCAGGTGCAACCAAACTACTTCTGGATGGTTCAGCGGTTGCGTGGAGCCCCCGGCCAGCT 1146
DB |||||
QY 1447 GCCAGGTGCAACCAAACTACTTCTGGATGGTTCAGCGGTTGCGTGGAGCCCCCGGCCAGCT 1506
DB |||||
QY 1147 GGAAGCCCCAGCAGATCCACCGCCAGAGAGCCCTTTATGATC 1189
DB |||||
QY 1507 GGAAGCCCCAGCAGATCCACCGCCAGAGAGCCCTTTATGACC 1549
DB |||||

RESULT 6
ADD29776
ID ADD29776 standard; mRNA; 2137 BP.
XX
AC ADD29776;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human tumour suppressor mRNA SEQ ID NO:234.
XX
KW ss; human; tumour suppressor; cancer; cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003058201-A2.
XX
PD 17-JUL-2003.
XX
PF 31-DEC-2002; 2002WO-US041825.
XX
PR 31-DEC-2001; 2001US-0345317P.
XX
PA (QUAR-) QUARK BIOTECH INC.
PA (CLEV-) CLEVELAND CLINIC FOUND.
XX
FI Feinstein E, Gudkov AV;
XX
DR WPI; 2003-598393/56.

XX Diagnosing cancer comprises determining the polypeptide or polynucleotide
 PT levels e.g., hepatic lipase, in a sample from a subject, where a higher
 PT level compared to that in a subject free of cancer is indicative of
 PT cancer.

PR 24-MAY-2002; 2002US-0392995P.
PR 31-MAY-2002; 2002US-0385023P.
PR 14-JUN-2002; 2002US-0388853P.
PR 17-JUN-2002; 2002US-0389395P.
PR 15-JUN-2002; 2002US-0391324P.
PR 25-JUL-2002; 2002US-0395944P.
PR 22-JUL-2002; 2002US-0397726P.
PR 13-AUG-2002; 2002US-0403046P.
PR 22-AUG-2002; 2002US-0405155P.
PR 27-AUG-2002; 2002US-0406361P.
PR 25-OCT-2002; 2002US-0421195P.
PR 12-NOV-2002; 2002US-0425456P.
PR 19-NOV-2002; 2002US-0427626P.
PR 10-DEC-2002; 2002US-0432122P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Hunter JJ, Macbeth KJ, Teai P, Lesoon A, Lightcap ES;
PI Williamson MW, Rudolph-Owen LA;
XX
XX WPI; 2003-646176/61.
DR P-PSDB; ADE38365.
XX
PT Treating subject having tumorigenic disorder or angiogenic disorder
PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
PT acid, by administering a modulator.
XX
XX
PS Disclosure; SEQ ID NO 25; 454bp; English.
XX
XX This invention relates to a novel method of treating a human subject
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC gene expression or activity of an isolated protein, by administering a
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC or ophthalmological activity. The method is useful for treating a subject
CC having a tumorigenic or angiogenic disorder, in particular for treating
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC present sequence is a DNA sequence which encodes the novel isolated human
CC protein 49863 of the invention.
XX
SQ Sequence 1799 BP; 304 A; 565 C; 588 G; 339 T; 0 U; 3 Other;

Query Match 96.9%; Score 1168.2; DB 10; Length 1799;
Best Local Similarity 99.2%; Pred. No. 6.3e-258;
Matches 1173; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 GGCACGAGGAGCGCGGTCCGAGGTTATGGATCCAGCGGCGGCGGCGGCGGTGCTCC 66
Db |||||
QY 67 CGCGGCCCTGCGCGTGTGCTGTGCTGAACCCCGCGCGGCGCAAGGCGCTTGC 126
Db 393 CGCGGCCCTGCGCGTGTGCTGTGCTGAACCCCGCGGCGGCAAGGCGCTTGC 452
QY 127 AGCTTTCGGAGTCACTGCGAGCCCTTTGGCTGAGGCTGAATCTCTTCAGCTGA 186
Db 453 AGCTTTCGGAGTCACTGCGAGCCCTTTGGCTGAGGCTGAATCTCTTCAGCTGA 512
QY 187 TGCTCACTGAGCGGCGGAACACGCGCGGAGCTGCTGCGTGGAGGAGCTGGGCGCT 246
Db 513 TGCTCACTGAGCGGCGGAACACGCGCGGAGCTGCTGCGTGGAGGAGCTGGGCGCT 572
QY 247 GGGACGCTCTGTGTGTCATGTCTGGAGACGGGCTGATGCAAGAGTGTGTGAACGGGCTCA 306
Db 573 GGGACGCTCTGTGTGTCATGTCTGGAGACGGGCTGATGCAAGAGTGTGTGAACGGGCTCA 632
QY 307 TGGAGCGGCTGACTGGGAGACGGGCTGATGCAAGAGCTGCTGAGCTCCAGAGGCT 366
Db 633 TGGAGCGGCTGACTGGGAGACGGGCTGATGCAAGAGCTGCTGAGCTCCAGAGGCT 692
QY 367 CTGGCAACCGCTGGCAGCTTCTTTGAACCAATTATGCTGGCTATGAGCAGGTCAACAATG 426
Db 693 CTGGCAACCGCTGGCAGCTTCTTTGAACCAATTATGCTGGCTATGAGCAGGTCAACAATG 752

QY 427 AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCGCGGCTGCTGTCAACCATGAC 486
Db |||||
QY 753 AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCGCGGCTGCTGTCAACCATGAC 812
Db |||||
QY 487 TGCTGTCTCTGCACACGGCTTCGGGGGCTGCGCCTTCTCTGTGCTCAGCCTGCGCTGGG 546
Db 813 TGCTGTCTCTGCACACGGCTTCGGGGGCTGCGCCTTCTCTGTGCTCAGCCTGCGCTGGG 872
QY 547 GCTTTCATTGCTGATGTGGACCTAGAGAGTGAGAAAGTATCGGCGTCTGGGGAGATGCGCT 606
Db 873 GCTTTCATTGCTGATGTGGACCTAGAGAGTGAGAAAGTATCGGCGTCTGGGGAGATGCGCT 932
QY 607 TCACCTGCGGCACTTCTGCTGCTGCGAGCTTGGGCACTTACCGCGGCGCAGCTGCGCT 666
Db 933 TCACCTGCGGCACTTCTGCTGCTGCGAGCTTGGGCACTTACCGCGGCGCAGCTGCGCT 992
QY 667 ACCTCCCTGTAGGAAGAGTGGTTCCCAAGACACCTGCTCCCGCTTGTGTGCTCAGCAGG 726
Db 993 ACCTCCCTGTAGGAAGAGTGGTTCCCAAGACACCTGCTCCCGCTTGTGTGCTCAGCAGG 1052
QY 727 GCCCGGTAGATGCACACCTTGTGCCACTTGGAGAGCAGTGCCTCTCACTTGGACAGTGG 786
Db 1053 GCCCGGTAGATGCACACCTTGTGCCACTTGGAGAGCAGTGCCTCTCACTTGGACAGTGG 1112
QY 787 TGCCCGGAGAGGACTTGTGCTAGTCTCTGGCACTGTGCTGCACTGCGCACTGGGCGAGTGA 846
Db 1113 TGCCCGGAGAGGACTTGTGCTAGTCTCTGGCACTGTGCTGCACTGCGCACTGGGCGAGTGA 1172
QY 847 TGTTTGTGCACCCATCGCGGCTGTCAGCTGCGGTCATGCATCTGTCTACCTGCGGG 906
Db 1173 TGTTTGTGCACCCATCGCGGCTGTCAGCTGCGGTCATGCATCTGTCTACCTGCGGG 1232
QY 907 CGGAGAGTCTCTGTCGCACTGCTGCGCCTTCTTCTGGCCATGAGAAGGCGAGGCATA 966
Db 1233 CGGAGAGTCTCTGTCGCACTGCTGCGCCTTCTTCTGGCCATGAGAAGGCGAGGCATA 1292
QY 967 TGGAGTATGAATGCCCTTACTTGTATATGTGCCCGTGGTGCCTTCCGCTTGGAGCCCA 1026
Db 1293 TGGAGTATGAATGCCCTTACTTGTATATGTGCCCGTGGTGCCTTCCGCTTGGAGCCCA 1352
QY 1027 AGGATGGAAAGTATGTTTGCAGTGGATGGGAATTGATGTTAGCGAGGCCCTGCAAG 1086
Db 1353 AGGATGGAAAGTATGTTTGCAGTGGATGGGAATTGATGTTAGCGAGGCCCTGCAAG 1412
QY 1087 GCCAGGTGCACCCAAACTACTTCTGGATGTTGAGCGTTCAGCGTGGAGCCCCGCCAGCT 1146
Db 1413 GCCAGGTGCACCCAAACTACTTCTGGATGTTGAGCGTTCAGCGTGGAGCCCCGCCAGCT 1472
QY 1147 GGAAGCCCCAGCAGATGCCACCGCCGCAAGAGCCCTTATGATC 1189
Db 1473 GGAAGCCCCAGCAGATGCCACCGCCGCAAGAGCCCTTATGATC 1515

RESULT 8
AAH16415
ID AAH16415 standard; cDNA; 1772 BP.
XX
AC AAH16415;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:15393.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
FN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 XX Primer sets for synthesising polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX Claim 8; SEQ ID NO 15393; 2537pp + Sequence Listing; English.
 XX The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 1772 BP; 285 A; 566 C; 585 G; 336 T; 0 U; 0 Other;
 Query Match 96.8%; Score 1167; DB 4; Length 1772;
 Best Local Similarity 99.2%; Pred. No. 1.2e-257;
 Matches 1173; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 7 GGCAAGAGAGCCCGGGTTCAGGTTATGATCCAGCGCGCGCCCCCGGGGGTGTCTCC 66
 DB 324 GGCAGCGGAGCGCGGGTTCAGGTTATGATCCAGCGCGCGCCCCCGGGGGTGTCTCC 383
 QY 67 CGCGGCCCTCGCGGTCTGCTGTGATACCGCGCGCGCGCGAGGCGCTTGC 126
 DB 384 CGCGGCCCTCGCGGTCTGCTGTGATACCGCGCGCGCGCGAGGCGCTTGC 443
 QY 127 AGCTTTCCGAGTCACTGTCAGCCCTTTTGGCTGAGGCTGAAATCTCTTCACTGCTGA 186
 DB 444 AGCTTTCCGAGTCACTGTCAGCGCCCTTTTGGCTGAGGCTGAAATCTCTTCACTGCTGA 503
 QY 187 TGCTCACTGAGCGCGGAAACCAACCGCGGAGCTGTGTGCGGTGCGAGAGCTGGCGGCT 246
 DB 504 TGCTCACTGAGCGCGGAAACCAACCGCGGAGCTGTGTGCGGTGCGAGAGCTGGCGGCT 563
 QY 247 GGGACGCTCTGGTGTGATGTCTGGAGACGGGCTGTGATGACAGAGTGTGTAAACGGGTCA 306
 DB 564 GGGACGCTCTGGTGTGATGTCTGGAGACGGGCTGTGATGACAGAGTGTGTAAACGGGTCA 623
 QY 307 TGGAGCGGCTGACTGGGAGACCGCCATCCAGAGCCCTGTGTAGCTCCACAGCGCT 366
 DB 624 TGGAGCGGCTGACTGGGAGACCGCCATCCAGAGCCCTGTGTAGCTCCACAGCGCT 683

QY 367 CTGGCAACGCGCTGGCAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCAACCAATG 426
 DB 684 CTGGCAACGCGCTGGCAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCAACCAATG 743
 QY 427 AAGACCTCTCTGACCAACTGCAAGCTATTGCTGTGCGCGCGGTGTGTACCCATGAACC 486
 DB 744 AAGACCTCTGACCAACTGCAAGCTATTGCTGTGCGCGCGGTGTGTACCCATGAACC 803
 QY 487 TGCTGTCTGTGACACAGCGCTTGGGGCTGGCGCTTCTTCTGTGTCTGAGCTGGCGCTGGG 546
 DB 804 TGCTGTCTGTGACACAGCGCTTGGGGCTGGCGCTTCTTCTGTGTCTGAGCTGGCGCTGGG 863
 QY 547 GCTTCATTGCTGATCTGGACCTTAGAGAGTGAGAACTATCGGCGTCTGGGGGAGATGCGCT 606
 DB 864 GCTTCATTGCTGATCTGGACCTTAGAGAGTGAGAACTATCGGCGTCTGGGGGAGATGCGCT 923
 QY 607 TCACCTCTGGGCACTTTTCTGCGCTCTGGCAGCTTGGCAGCTTACCGCGCGCCGACCTGGCT 666
 DB 924 TCACCTCTGGGCACTTTTCTGCGCTCTGGCAGCTTGGCAGCTTACCGCGCGCCGACCTGGCT 983
 QY 667 ACCTCCCTGTAGGAAGAGTGGGTTCCAGACACCTGCTCCCGCTTGTGGTCCAGCAGG 726
 DB 984 ACCTCCCTGTAGGAAGAGTGGGTTCCAGACACCTGCTCCCGCTTGTGGTCCAGCAGG 1043
 QY 727 GCGCGGTAGATGCACACCTTGTGCCACTGGAGAGCAGTGCCTCTCACTGGACAGTGG 786
 DB 1044 GCGCGGTAGATGCACACCTTGTGCCACTGGAGAGCAGTGCCTCTCACTGGACAGTGG 1103
 QY 787 TGCCCGAGCAGAGACTTTTGTGTAGTCTGGCACTGCTGCACCTCGCACTGGGCGAGTGAGA 846
 DB 1104 TGCCCGAGCAGAGACTTTTGTGTAGTCTGGCACTGCTGCACCTCGCACTGGGCGAGTGAGA 1163
 QY 847 TGTGTGTGCACACCATGGGCGCTGTGCAGCTGGGCTCATGATCTGTCTAGCTGGGG 906
 DB 1164 TGTGTGTGCACACCATGGGCGCTGTGCAGCTGGGCTCATGATCTGTCTAGCTGGGG 1223
 QY 907 CGGGAGTGTCTGTCGCATGCTGCGCTCTTCTGCGCATGGAGAAGGGCAGGCATA 966
 DB 1224 CGGGAGTGTCTGTCGCATGCTGCGCTCTTCTGCGCATGGAGAAGGGCAGGCATA 1283
 QY 967 TGGAGTATGAATGCCCTACTTTGGTATATGTGCCGTGCTGCGCTTCCCTTGGAGCCCA 1026
 DB 1284 TGGAGTATGAATGCCCTACTTTGGTATATGTGCCGTGCTGCGCTTCCCTTGGAGCCCA 1343
 QY 1027 AGATGGGAAAGGTATGTTTGCAGTGGATGGGAATTGATGTTAGCGAGGCGCTGCAGG 1086
 DB 1344 AGATGGGAAAGGTATGTTTGCAGTGGATGGGAATTGATGTTAGCGAGGCGCTGCAGG 1403
 QY 1087 GTCAGGTGACCCCAACTACTTCTGGATGCTCAGCGGTTGCGTGGAGCCCCCGGCCAGCT 1146
 DB 1404 GTCAGGTGACCCCAACTACTTCTGGATGCTCAGCGGTTGCGTGGAGCCCCCGGCCAGCT 1463
 QY 1147 GGAAGCCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1189
 DB 1464 GGAAGCCCCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1506
 RESULT 9
 ID ADQ17904 standard; DNA; 1783 BP.
 XX ADQ17904;
 XX ADQ17904;
 DT 25-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 721.
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.
 XX Homo sapiens.
 OS

PN W02004048938-A2.
 XX 10-JUN-2004.
 PD 26-NOV-2003; 2003WO-US038193.
 XX 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 XX Aziz N, Ginsburg WM, Zlotnik A;
 XX WPI; 2004-441208/41.
 DR
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 721; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytotstatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC DNA of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 1783 BP; 314 A; 546 C; 591 G; 332 T; 0 U; 0 Other;

Query Match 96.5%; Score 1162.6; DB 12; Length 1783;
 Best Local Similarity 98.4%; Pred. No. 1.2e-256;
 Matches 1174; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGCACGAGGAGCGCGGGTCGAGGTATGATTCACGCGGGCGGGCGCGGTCTCC 66
 DB 311 GGCACGAGGAGCGCGGGTCGAGGTATGATTCACGCGGGCGGGCGGTCTCC 370
 QY 67 CGCGGCCCTGCGCGGTGCTGCTGCTGAACCCCGCGCGGGCAAGGCGCTTGC 126
 DB 371 CGCGGCCCTGCGCGGTGCTGCTGCTGAACCCCGCGCGGGCAAGGCGCTTGC 430
 QY 127 AGCTCTTCGGAGTACGTCGAGCCCTTTGGCTGAGGCTGAATCTCCTTCAGCTGA 186
 DB 431 AGCTCTTCGGAGTACGTCGAGCCCTTTGGCTGAGGCTGAATCTCCTTCAGCTGA 490
 QY 187 TGCTCACTGAGCGCGGAACACGCGCGGAGCTGGTGGCTGCGGAGGAGCTGGGCCGCT 246
 DB 491 TGCTCACTGAGCGCGGAACACGCGCGGAGCTGGTGGCTGCGGAGGAGCTGGGCCGCT 550
 QY 247 GGGACGCTCTGTGTGTCATGTCTGGAGACGGGCTCATGACGAGTGTGTGAACGGGCTCA 306
 DB 551 GGGACGCTCTGTGTGTCATGTCTGGAGACGGGCTCATGACGAGTGTGTGAACGGGCTCA 610
 QY 307 TGGAGGGGCTTACTGGGAGACCGGCATCCAGAGCCCTGTGTAGCTCCCGAGGAGCT 366
 DB 611 TGGAGGGGCTTACTGGGAGACCGGCATCCAGAGCCCTGTGTAGCTCCCGAGGAGCT 670
 QY 367 CTGGCAACCGCTGGCAGCTTCTCTTGAACCATATGCTGGCTATGAGCAGGTCACCAATG 426
 DB 671 CTGGCAACCGCTGGCAGCTTCTCTTGAACCATATGCTGGCTATGAGCAGGTCACCAATG 730
 QY 427 AAGACCTCTGACCAACATGACGCTATTGCTGTGCGCGGCTGTGTACCCATGAACC 486
 DB 731 AAGACCTCTGACCAACATGACGCTATTGCTGTGCGCGGCTGTGTACCCATGAACC 790

QY 487 TGCTGTCTCTGCACACGCGTTCGGGGCTGGCCCTCTTCTCTGTGCTCAGCCTGGCCCTGGG 546
 DB 791 TGCTGTCTCTGCACACGCGTTCGGGGCTGGCCCTCTTCTCTGTGCTCAGCCTGGCCCTGGG 850
 QY 547 GCTTCATTGTCTGATGTGGACCTAGAGAGTGAAGATATCGCGCTGTGGGGAGATGCGCT 606
 DB 851 GCTTCATTGTCTGATGTGGACCTAGAGAGTGAAGATATCGCGCTGTGGGGAGATGCGCT 910
 QY 607 TCACCTTGGGCACCTTCTCGGCTCTGCGACCTTGGCAGCTTACCGGGCCGACCTGGCTT 666
 DB 911 TCACCTTGGGCACCTTCTCGGCTCTGCGACCTTGGCAGCTTACCGGGCCGACCTGGCTT 970
 QY 667 ACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCTCCCGCTGTGTGTCTCCAGCAGG 726
 DB 971 ACCTCCCTGTAGGAAGAGTGGTTCCAAAGACACCTGCTCCCGCTGTGTGTCTCCAGCAGG 1030
 QY 727 GCCCGGTAGATGCACACCTTGTGCCACTTGGAGGAGCCAGTGCCCTCTCCTTGGACAGTGG 786
 DB 1031 GCCCGGTAGATGCACACCTTGTGCCACTTGGAGGAGCCAGTGCCCTCTCCTTGGACAAATGG 1090
 QY 787 TGCCCGAGGAGGACTTGTGTAGTCTCTGGCACTGTGCACTCGCACTGGGCACTGAGAGA 846
 DB 1091 TGCCCGAGGAGGACTTGTGTAGTCTCTGGCACTGTGCACTCGCACTGGGCACTGAGAGA 1150
 QY 847 TGTGTTGCTGCACCCATCGGCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACCTGCGGG 906
 DB 1151 TGTGTTGCTGCACCCATCGGCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACCTGCGGG 1210
 QY 907 CGGAGGTGCTCTGTCGCCATGCTGCTGCGCTCTTCTTGCCCATGGAGAAGGCGCAGGCATA 966
 DB 1211 CGGAGGTGCTCTGTCGCCATGCTGCTGCGCTCTTCTTGCCCATGGAGAAGGCGCAGGCATA 1270
 QY 967 TGGAGTATGAATGCCCTTACTTGTATATGTGCCCGTGGTGGCTTCCGCTTGGAGGCCCA 1026
 DB 1271 TGGAGTATGAATGCCCTTACTTGTATATGTGCCCGTGGTGGCTTCCGCTTGGAGGCCCA 1330
 QY 1027 AGGATGGGAAGGTATGTTTGCAGTGGTGGGAATGATGTTAGCGAGGCCGTGCGAGG 1086
 DB 1331 AGGATGGGAAGGTATGTTTGCAGTGGTGGGAATGATGTTAGCGAGGCCGTGCGAGG 1390
 QY 1087 GCCAGGTGCAACCCAACTACTTCTGGATGGTTCAGCGGTGCGTGGAGCCCCCGCCAGCT 1146
 DB 1391 GCCAGGTGCAACCCAACTACTTCTGGATGGTTCAGCGGTGCGTGGAGCCCCCGCCAGCT 1450
 QY 1147 GGAAGCCCCCAGCAGATGCCACCGCCAGAGCCCTTATGATCTAGAGTCGAC 1199
 DB 1451 GGAAGCCCCCAGCAGATGCCACCGCCAGAGCCCTTATGATCTAGAGTCGAC 1503

RESULT 10
 AAV84490
 ID AAV84490 standard; DNA; 1533 BP.
 XX
 AC AAV84490;
 XX
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Human secreted protein gene 80 clone HNPAB54.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; da;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 XX
 FN W09854963-A2.
 XX
 PD 10-DEC-1998.

QY 306 ATGGAGCGCGCTGACTGGGAGACCGCCATCCAGAAAGCCCTGTGTAGCTCCAGCAGGC 365
 Db |||||
 QY 347 ATGGAGCGCGCTGACTGGGAGACCGCCATCCAGAAAGCCCTGTGTAGCTCCAGCAGGC 406
 Db |||||
 QY 366 TCTGGCAACGCGCTGGCAGCTTCTTGTGAACCAATTATGCTGGCTATGACGAGTCAACCAAT 425
 Db |||||
 QY 407 TCTGGCAACGCGCTGGCAGCTTCTTGTGAACCAATTATGCTGGCTATGACGAGTCAACCAAT 466
 QY 426 GAAGACCTCTTACCAACTGACGCTATTTGCTGTGCGCGCGGCTGCTGACCCATGAAC 485
 Db |||||
 QY 467 GAAGACCTCTTACCAACTGACGCTATTTGCTGTGCGCGCGGCTGCTGACCCATGAAC 526
 QY 486 CTGCTGTCTCTGCACACGCGCTTTCGGGGCTGCGCCCTCTTCTGTGCTCAGCCTGCGCTGG 545
 Db |||||
 QY 527 CTGCTGTCTCTGCACACGCGCTTTCGGGGCTGCGCCCTCTTCTGTGCTCAGCCTGCGCTGG 586
 QY 546 GGCCTTCATTGTGTGTGGACCTAGAGAGTGAGAAAGTATCGCGCTTCGGGGAGATGCGC 605
 Db |||||
 QY 587 GGCCTTCATTGTGTGTGGACCTAGAGAGTGAGAAAGTATCGCGCTTCGGGGAGATGCGC 646
 QY 606 TTCACCTCTGGGCACCTTCTGCGCTTTCGGCAGCCTTTCGGCAGCTTACCGCGCGCAGTGCCT 665
 Db |||||
 QY 647 TTCACCTCTGGGCACCTTCTGCGCTTTCGGCAGCCTTTCGGCAGCCTTACCGCGCGCAGTGCCT 706
 QY 666 TACCTCCCTGTAGGAAGAGTGGGTTTCCAAGACACCTGCTCCCGCGTTGTGTCCAGCAG 725
 Db |||||
 QY 707 TACCTCCCTGTAGGAAGAGTGGGTTTCCAAGACACCTGCTCCCGCGTTGTGTCCAGCAG 766
 QY 726 GCGCCGGTAGATGCAACCTTGTGCGACTGGAGGAGCCAGTGCCTCTCACTGGACAGTG 785
 Db |||||
 QY 767 GCGCCGGTAGATGCAACCTTGTGCGACTGGAGGAGCCAGTGCCTCTCACTGGACAGTG 826
 QY 786 GTGCCCGAGGAGACTTGTGTAGTCTGCGACCTGCTGCACTGCGACCTGCGGAGTGCAG 845
 Db |||||
 QY 827 GTGCCCGAGGAGACTTGTGTAGTCTGCGACCTGCTGCACTGCGACCTGCGGAGTGCAG 886
 QY 846 ATGTTTGTGTGCAACCATGGCGCGTGTGCAGCTGGCGTCACTGCTTCTACGTGCGG 905
 Db |||||
 QY 887 ATGTTTGTGTGCAACCATGGCGCGTGTGCAGCTGGCGTCACTGCTTCTACGTGCGG 946
 QY 906 GCGGAGTGTTCGTGCCATGCTGTGCGCCTCTTCTTGCCCATGAGAGGCGCAGGCAAT 965
 Db |||||
 QY 947 GCGGAGTGTTCGTGCCATGCTGTGCGCCTCTTCTTGCCCATGAGAGGCGCAGGCAAT 1006
 QY 966 ATGGATATGAATGCCCTTACTTGTGTATATGTCGCCGTGCTGCGCTTCCGCTTGAGGCC 1025
 Db |||||
 QY 1007 ATGGATATGAATGCCCTTACTTGTGTATATGTCGCCGTGCTGCGCTTCCGCTTGAGGCC 1066
 QY 1026 AAGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTGATGTTAGCGAGCGCGTGCGAG 1085
 Db |||||
 QY 1067 AAGGATGGGAAAGGTATGTTTGCAGTGGATGGGAAATTGATGTTAGCGAGCGCGTGCGAG 1126
 QY 1086 GCGCAGGTGCACCCAACTACTTCTGGATGTTGCGGTTGCGTGGAGCCCGCCCGCCAGC 1145
 Db |||||
 QY 1127 GCGCAGGTGCACCCAACTACTTCTGGATGTTGCGGTTGCGTGGAGCCCGCCCGCCAGC 1186
 QY 1146 TGGAGCCCGCAGCAGATGCCACCGCAGAGAGCCCTTATGATC 1189
 Db |||||
 QY 1187 TGGAGCCCGCAGCAGATGCCACCGCAGAGAGCCCTTATGACC 1230

RESULT 11

ABAB3273
 ID ABAB3273 standard; cDNA; 1533 BP.

XX AC ABAB3273;

XX DT 07-FEB-2002 (first entry)

XX DE Human secreted protein gene 80 SEQ ID NO:90.

XX KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;

KW cytotstatic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulneryary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; chromosome 17; ss.

XX Homo sapiens.

XX WO200162891-A2.

XX 30-AUG-2001.

XX 21-FEB-2001; 2001WO-US005614.

XX 24-FEB-2000; 2000US-0184836P.

XX 29-MAR-2000; 2000US-0193170P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;

XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;

XX Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;

XX Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z;

XX Greene JM;

XX WPI; 2001-625724/72.

XX P-PSDB; ABB50380.

XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
 and diabetic retinopathy.

XX Claim 1; Page 965; 1533pp; English.

XX ABB50301 to ABB51287 and ABB5194 to ABB53441 represent human secreted
 proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytotstatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulneryary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABB5185 to
 CC ABB53193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention
 XX

XX Sequence 1533 BP; 272 A; 454 C; 495 G; 302 T; 0 U; 10 Other;

Query Match 95.4%; Score 1149.4; DB 4; Length 1533;

Best Local Similarity 98.3%; Pred. No. 1.2e-253;

Matches 1164; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 7 GGCACGAGGAGCCCGCGGTTCGAGGTATGATCCAGCGGCGGCCCGCGGCGGTGTCTCC 66

Db |||||

Db 47 GGCAGCGGAGCCCGCGGTTCGAGGTATGATCCAGCGGCGGCCCGCGGCGGTGTCTCC 106

QY 67 CGCGGCGCTGCGCGTGTCTGTGTAACCCCGCGGCGGCAAGGCAAGCCTTGC 126

Db |||||

Db 107 CGCGGCGCTGCGGTGCTGTGTAACCCCGCGGCGGCAAGGCAAGCCTTGC 166

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QY 127 AGCTCTTCGGAGTCACGTGCGAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGA 186
Db 167 AGCTCTTCGGAGTCACGTGCGAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGA 226
QY 187 TGCCTCACTGAGCGGCGGAACACGCGCGGAGCTGCTGCGTCCGAGGAGCTGGGCCGCT 246
Db 227 TGCCTCACTGAGCGGCGGAACACGCGCGGAGCTGCTGCGTCCGAGGAGCTGGGCCGCT 286
QY 247 GGGAGCGCTGTGTGTGTCATGTCTGGAGACGGGCTGATGCAACAGGTGTGTGAACGGGC-TC 305
Db 287 GGRACGCTCTGTGTGTGTCATGTCTGGAGACGGGCTGATGCAACAGGTGTGTGAACGGGCTTC 346
QY 306 ATGGAGCGGCTGACTGGGAGACCGCATCCAGAGCCCTCTGTGTAGCTCCACGAGCGC 365
Db 347 ATGGAGCGGCTGACTGGGAGACCGCATCCAGAGCCCTCTGTGTAGCTCCACGAGCGC 406
QY 366 TCTGGCAACGCGCTGGCAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCAACCAAT 425
Db 407 TCTGGCAACGCGCTGGCAGCTTCTTGAACCAATTATGCTGGCTATGAGCAGGTCAACCAAT 466
QY 426 GAAGACCTCTGACCAACTGCAAGCTATTTGCTGTGCGCGCGGCTGTGTCAACCATGAAC 485
Db 467 GAAGACCTCTGACCAACTGCAAGCTATTTGCTGTGCGCGCGGCTGTGTCAACCATGAAC 526
QY 486 CTGCTGTCTGTGACACGCGCTTGGGGCTGCGGCTCTTCTGTGCTCAGCGCTGGCTGG 545
Db 527 CTGCTGTCTGTGACACGCGCTTGGGGCTGCGGCTCTTCTGTGCTCAGCGCTGGCTGG 586
QY 546 GCGTTCAATGCTGATGTGACCTTAGAGAGTGAGAGTATCGGCGTCTGGGGGAGATGCGC 605
Db 587 GCGTTCAATGCTGATGTGACCTTAGAGAGTGAGAGTATCGGCGTCTGGGGGAGATGCGC 646
QY 606 TTCACCTCTGGGCACTTTCCTGCGTCTGGCAGCCTTCGCGCACTTACCGCGGCGCACTGGCT 665
Db 647 TTCACCTCTGGGCACTTTCCTGCGTCTGGCAGCCTTCGCGCACTTACCGCGGCGCACTGGCC 706
QY 666 TACCTCCCTGTAGGAAGTGGTGTCAAGACACTGCGCTCCCGCTTGTGTCCAGCAG 725
Db 707 TACCTCCCTGTAGGAAGTGGTGTCAAGACACTGCGCTCCCGCTTGTGTCCAGCAG 766
QY 726 GCGCCGCTAGATGCACACCTTGTGCGCTAGTGGAGGCGAGTGCCTCTCACTGGACAGTG 785
Db 767 GCGCCGCTAGATGCACACCTTGTGCTAGTGGAGGCGAGTGCCTCTCACTGGACAGTG 826
QY 786 GTGCCCGACGAGGACTTGTGTAGTCTGGCACTGCTGCACTCGCACTCGGCACTGGGCACTGAG 845
Db 827 GTGCCCGACGAGGACTTGTGTAGTCTGGCACTGCTGCACTCGGCACTGGGCACTGAG 886
QY 846 ATGTTTGTGCAACCAATGGGCGGCTGTGAGCTGGGCTCATGCACTGTCTTACGTGCGG 905
Db 887 ATGTTTGTGCAACCAATGGGCGGCTGTGAGCTGGGCTCATGCACTGTCTTACGTGCGG 946
QY 906 GCGGAGTGTCTGTCGATGCTGCTGCGCTCTTCTGCGCATGAGAGGAGGCGAGCAT 965
Db 947 GCGGAGTGTCTGTCGATGCTGCTGCGCTCTTCTGCGCATGAGAGGAGGCGAGCAT 1006
QY 966 ATGGAGTATGAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCGCTTTGGAGCCC 1025
Db 1007 ATGGAGTATGAATGCCCTACTTGGTATATGTGCGCGTGTGCGCTTCGCTTTGGAGCCC 1066
QY 1026 AAGATGGGAAGATAGTTTGAAGTGGATGGGAATTGATGTTAGCGAGGCGCGCTGCAG 1085
Db 1067 AAGATGGGAAGATAGTTTGAAGTGGATGGGAATTGATGTTAGCGAGGCGCGCTGCAG 1126
QY 1086 GGCAGGTGCACCAACTACTTCTGATGCTGAGCGGTTGCGTGGAGCCCGCCCGCAGC 1145
Db 1127 GGCAGGTGCACCAACTACTTCTGATGCTGAGCGGTTGCGTGGAGCCCGCCCGCAGC 1186
QY 1146 TGAAGCGCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1189
Db 1187 TGAAGCGCCAGCAGATGCCACCGCCAGAGAGCCCTTATGATC 1230
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RESULT 12
ACH04774
ID ACH04774 standard; cDNA; 1533 BP.
XX
AC ACH04774;
XX
DT 02-OCT-2003 (first entry)
XX
DE Novel human secreted protein #80 cDNA.
XX
KW Human; ss; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
systemic lupus erythematosus; haematopoietic cell disorder; allergy;
agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder;
afibrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis;
inflammatory condition; ischaemia-reperfusion injury; infectious disease;
hyperproliferative disorder; purpura; viral infection; regeneration;
bacterial infection; ulcer; Alzheimer's disease; gene.
XX
OS Homo sapiens.
XX
PN US2003065160-A1.
XX
PD 03-APR-2003.
XX
PF 07-DEC-2001; 2001US-00004860.
XX
PR 06-JUN-1997; 97US-0048875P.
PR 06-JUN-1997; 97US-0048876P.
PR 06-JUN-1997; 97US-0048877P.
PR 06-JUN-1997; 97US-0048878P.
PR 06-JUN-1997; 97US-0048880P.
PR 06-JUN-1997; 97US-0048881P.
PR 06-JUN-1997; 97US-0048882P.
PR 06-JUN-1997; 97US-0048883P.
PR 06-JUN-1997; 97US-0048884P.
PR 06-JUN-1997; 97US-0048885P.
PR 06-JUN-1997; 97US-0048892P.
PR 06-JUN-1997; 97US-0048893P.
PR 06-JUN-1997; 97US-0048894P.
PR 06-JUN-1997; 97US-0048895P.
PR 06-JUN-1997; 97US-0048896P.
PR 06-JUN-1997; 97US-0048897P.
PR 06-JUN-1997; 97US-0048898P.
PR 06-JUN-1997; 97US-0048899P.
PR 06-JUN-1997; 97US-0048900P.
PR 06-JUN-1997; 97US-0048901P.
PR 06-JUN-1997; 97US-0048915P.
PR 06-JUN-1997; 97US-0048916P.
PR 06-JUN-1997; 97US-0048917P.
PR 06-JUN-1997; 97US-0048949P.
PR 06-JUN-1997; 97US-0048962P.
PR 06-JUN-1997; 97US-0048963P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048970P.
PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0048974P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.
PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
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Best Local Similarity 98.3%; Pred. No. 1.2e-253;
Matches 1164; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

Qy	7	GGC	ACG	GAG	AGC	CGG	GT	CAG	GGT	TAT	TGG	ATC	CAG	GGG	CGG	CCG	CCG	CGG	CGT	TG	TCC	66
Db	47	GGC	ACG	GGG	AGC	CGG	GT	CAG	GGT	TAT	TGG	ATC	CAG	GGG	CGG	CCG	CCG	CGG	CGT	TG	TCC	108
Qy	67	CGC	GGC	CTT	CGG	AGT	CAG	TG	CTG	CTG	TGA	ACC	CGC	GGG	CGG	CAA	GGG	CAAG	GC	CTT	TGC	126
Db	107	CGC	GGC	CTT	CGG	TG	CTG	CTG	TGA	ACC	CGC	GGG	CGG	CAA	GGG	CAAG	GC	CTT	TGC	CTT	TGC	166
Qy	127	AGC	CTT	CTT	CGG	AGT	CAG	TG	CAG	CCC	CTT	TTT	GGC	TG	AGG	CT	GAA	AT	CT	CTT	TC	186
Db	167	AGC	CTT	CTT	CGG	AGT	CAG	TG	CAG	CCC	CTT	TTT	GGC	TG	AGG	CT	GAA	AT	CT	CTT	TC	226
Qy	187	TG	CTC	ACT	GAG	CGG	CGG	AG	CA	CCG	GGG	AG	CT	TG	TG	CGT	CGG	AG	CA	GGT	CG	246
Db	227	TG	CTC	ACT	GAG	CGG	CGG	AG	CA	CCG	GGG	AG	CT	TG	TG	CGT	CGG	AG	CA	GGT	CG	286
Qy	247	GGG	ACG	CTT	CGT	CGT	CAT	GT	CTG	GAC	CGG	CGT	GAT	GCA	CG	AGT	TG	TGA	AC	GGC	CT	305
Db	287	GGG	ACG	CTT	CGT	CGT	CAT	GT	CTG	GAC	CGG	CGT	GAT	GCA	CG	AGT	TG	TGA	AC	GGC	CT	346
Qy	306	ATG	GAG	CGG	CGT	GAT	CTG	GAG	ACG	CCCAT	CCAG	AAG	CCCT	TG	TG	TAG	CGCT	CCCC	ACG	AGC	365	
Db	347	ATG	GAG	CGG	CGT	GAT	CTG	GAG	ACG	CCCAT	CCAG	AAG	CCCT	TG	TG	TAG	CGCT	CCCC	ACG	AGC	406	
Qy	366	TCT	GGC	AA	CGG	CTT	GGG	AG	CTT	CTT	TGA	CA	ATT	TAT	GT	TG	CT	AT	GAG	CA	GGT	425
Db	407	TCT	GGC	AA	CGG	CTT	GGG	AG	CTT	CTT	TGA	CA	ATT	TAT	GT	TG	CT	AT	GAG	CA	GGT	466
Qy	426	GAG	AC	CTT	CTG	AC	CA	CTG	CA	CGT	AT	TG	CTG	TG	CGC	CGC	GT	CT	GAT	CA	CCAT	485
Db	467	GAG	AC	CTT	CTG	AC	CA	CTG	CA	CGT	AT	TG	CTG	TG	CGC	CGC	GT	CT	GAT	CA	CCAT	526
Qy	486	CTG	CT	GT	CTT	CTG	AC	AC	GGC	TT	CGG	GGT	TG	CGC	CT	CTT	CT	TG	TG	CT	CAG	545
Db	527	CTG	CT	GT	CTT	CTG	AC	AC	GGC	TT	CGG	GGT	TG	CGC	CT	CTT	CT	TG	TG	CT	CAG	586
Qy	546	GGC	TT	CA	TG	TG	TG	TG	GG	AG	CT	TAG	AG	TG	TG	AG	AG	AT	TG	GG	GGG	605
Db	587	GGC	TT	CA	TG	TG	TG	TG	GG	AG	CT	TAG	AG	TG	TG	AG	AG	AT	TG	GG	GGG	646
Qy	606	TT	CA	CT	CTG	GG	CA	CTT	CT	CG	CT	TG	CG	CA	CTT	AC	CG	CGC	CG	CA	CT	665
Db	647	TT	CA	CT	CTG	GG	CA	CTT	CT	CG	CT	TG	CG	CA	CTT	AC	CG	CGC	CG	CA	CT	706
Qy	666	TAC	CT	CC	CT	TG	TG	AG	AG	TG	GG	TT	CCA	AG	CA	CT	CG	CT	CC	CG	CT	725
Db	707	TAC	CT	CC	CT	TG	TG	AG	AG	TG	GG	TT	CCA	AG	CA	CT	CG	CT	CC	CG	CT	766
Qy	726	GGC	CGG	TAG	AT	G	CAC	ACT	TG	TG	GC	CA	CTG	GAG	GAC	CA	TG	CC	CT	CA	TG	785
Db	767	GGC	CGG	TAG	AT	G	CAC	ACT	TG	TG	GC	CA	CTG	GAG	GAC	CA	TG	CC	CT	CA	TG	826
Qy	786	GT	CC	CG	AC	GAG	CA	CTT	TG	CT	AG	CT	CG	CA	CTT	G	C					845
Db	827	GT	CC	CG	AC	GAG	CA	CTT	TG	CT	AG	CT	CG	CA	CTT	G	C					886
Qy	846	AT	G	T	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	905
Db	887	AT	G	T	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	946
Qy	906	GCG	GAG	TG	CT	G	T	G	C	C	A	T	G	T	G	C	C	A	T	G	C	965
Db	947	GCG	GAG	TG	CT	G	T	G	C	C	A	T	G	T	G	C	C	A	T	G	C	1006
Qy	966	AT	GAG	T	AT	GA	T	GC	CC	CT	ACT	TG	T	AT	G	T	G	C	C	CT	1025	
Db	1007	AT	GAG	T	AT	GA	T	GC	CC	CT	ACT	TG	T	AT	G	T	G	C	C	CT	1066	
Qy	1026	AAG	GAT	GGG	AA	GAG	T	AT	G	T	T	G	C	AG	T	G	GG	AA	T	AT	G	1085

Db	1067	AAGATCGGAAAGGTGTGTTGGCAGTGGATGGGGAATTGATGGTTAGCAGGCCGTGCAG	1182
Qy	1086	GGCCAGGTGCACCAAACTACTTTCTGGATGGTTCAGCGGTTGCGTGGAGCCCCCGCCAGC	1145
Db	1127	GGCAGGTGCACCAAACTACTTTCTGGATGGTTCAGCGGTTGCGTGGAGCCCCCGCCAGC	1186
Qy	1146	TGGAAAGCCCCAGCAGATGCCACGCCAGAAAGAGCCCTTATGATC	1189
Db	1187	TGGAAAGCCCCAGCAGATGCCACGCCAGAAAGAGCCCTTATGACC	1230
RESULT 14			
ABK90198	ID	ABK90198 standard; cDNA; 1155 BP.	
XX	AC	ABK90198;	
XX	DT	05-NOV-2002 (first entry)	
XX	DE	cDNA encoding human sphingosine kinase 1 (SPHK1).	
XX	KW	Human; sphingosine kinase 1; SPHK1; blood vessel formation; primate;	
KW	KW	congestive heart failure; myocardial ischaemia; wound healing;	
KW	KW	ischaemia-reperfusion injury; peripheral arterial disease; angiogenesis;	
KW	KW	coronary artery disease; peripheral vascular disease; fracture repair;	
KW	KW	reconstructive surgery; transplantation; islet transplant; tendon repair;	
KW	KW	sports injury; ulcer; thromboangitis obliterans; Buerger's disease; gene;	
KW	KW	periodontal tissue regeneration; radiotherapy-induced oesophagitis; ss.	
OS		Homo sapiens.	
XX	Key	Location/Qualifiers	
FH	CDS	1..1155	
FT		/*tag= a	
FT		/product= "Human sphingosine kinase 1 (SPHK1) "	
XX			
FN	WO200228406-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-EP011513.		
XX			
PR	05-OCT-2000; 2000US-0238230P.		
XX			
PA	(NOVS) NOVARTIS AG.		
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX			
PI	Liau G, Stefansson S, Su J;		
XX			
DR	WPI; 2002-608171/65.		
DR	P-PSDB; ABG31586.		
XX			
PT	Inducing blood vessel formation, or preventing/treating congestive heart		
PT	failure, ischaemia-reperfusion injury, myocardial ischemia and peripheral		
PT	arterial diseases in animal, by administering sphingosine kinase.		
XX			
PS	Disclosure; Page 33-34; 45pp; English.		
XX			
CC	The present invention relates to a new method of inducing blood vessel		
CC	formation in an animal. The method of the invention involves		
CC	administering sphingosine kinase to the animal. The method is useful for		
CC	inducing blood vessel formation in an animal, or preventing or treating		
CC	congestive heart failure, myocardial ischaemia, ischaemia-reperfusion		
CC	injury and peripheral arterial diseases in an animal, e.g. mammal (such		
CC	as primate including human). The invention is also useful for treating		
CC	diseases or disorders selected from coronary artery disease, peripheral		
CC	vascular disease, wound healing and fracture repair, reconstructive		
CC	surgery, transplantation such as islet transplants, tendon repair/sports		
CC	injury, healing of ulcers, thromboangitis obliterans (Buerger's disease),		
CC	periodontal tissue regeneration and radiotherapy-induced oesophagitis.		
CC	The present nucleic acid sequence encodes the human sphingosine kinase 1		
XX	(SPHK1) protein as described in the invention		
XX			

SQ	Sequence	1155 BP; 185 A; 349 C; 382 G; 239 T; 0 U; 0 Other;
	Query Match	95.2%; Score 1147; DB 6; Length 1155;
	Best Local Similarity	99.6%; Pred. No. 4,2e-253;
	Matches 1150; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	33	ATGGATCCAGCGGGGGCCCCCGGGCGTGTCCCGCGCCCTGCGCGGTGCTGTGTGCTG 92
DB	1	ATGGATCCAGCGGGGGGGCCCCCGGGCGTGTCCCGCGCCCTGCGCGGTGCTGTGTGCTG 60
QY	93	CTGAACCCCGCGGGCGGCAAGGCTTTGCAAGCTCTTCCGAGTCACTGCGAGCCC 152
DB	61	CTGAACCCCGCGGGCGGCAAGGCTTTGCAAGCTCTTCCGAGTCACTGCGAGCCC 120
QY	153	CTTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGGGGGGAACACGG 212
DB	121	CTTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGGGGGGAACACGG 180
QY	213	CGGGAGCTGCTGGGTGCGAGAGCTGGGCGCTGGAGCGCTCTGGTGTCTATGCTGGA 272
DB	181	CGGGAGCTGCTGGGTGCGAGAGCTGGGCGCTGGAGCGCTCTGGTGTCTATGCTGGA 240
QY	273	GACGGCTGATGACAGAGTGTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCC 332
DB	241	GACGGCTGATGACAGAGTGTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCC 300
QY	333	ATCCAGAAGCCCTGTGTAGCTTCCAGCAGGCTCTGGCAACCGCTGCGAGCTTCCCTTG 392
DB	301	ATCCAGAAGCCCTGTGTAGCTTCCAGCAGGCTCTGGCAACCGCTGCGAGCTTCCCTTG 360
QY	393	AACCATATGCTGGCTATGAGAGGTGACCAATGAGAGCTCTCTGACCAACTGCAGCTA 452
DB	361	AACCATATGCTGGCTATGAGAGGTGACCAATGAGAGCTCTCTGACCAACTGCAGCTA 420
QY	453	TTGCTGTGCGCGGCTGTGTCAACCATGAACCTGCTGTCTGTGACACGCGCTTCGGGG 512
DB	421	TTGCTGTGCGCGGCTGTGTCAACCATGAACCTGCTGTCTGTGACACGCGCTTCGGGG 480
QY	513	CTGCGCTCTTCTGTGTGTGCTGAGCTTGGCTTGGGGCTTCAATGCTGATGTGACCTAGAG 572
DB	481	CTGCGCTCTTCTGTGTGTGCTGAGCTTGGCTTGGGGCTTCAATGCTGATGTGACCTAGAG 540
QY	573	AGTGAGAGTATCGGCGTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTCTG 632
DB	541	AGTGAGAGTATCGGCGTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTCGCTCTG 600
QY	633	GCAGCCTTGGCGCACTTACCGCGCGCGACTGGCTTACTCTCTAGGAAAGATGGGTTC 692
DB	601	GCAGCCTTGGCGCACTTACCGCGCGCGACTGGCTTACTCTCTAGGAAAGATGGGTTC 660
QY	693	AAGACACCTGCTCCCGCTTGTGTGTCAGAGGGCCCGGTAGATGACACCTTGTGCGCA 752
DB	661	AAGACACCTGCTCCCGCTTGTGTGTCAGAGGGCCCGGTAGATGACACCTTGTGCGCA 720
QY	753	CTGGAGGAGCAGTGCCTCTCACTGACAGTGGTCCCGACGAGCACTTTGTGCTAGTC 812
DB	721	CTGGAGGAGCAGTGCCTCTCACTGACAGTGGTCCCGACGAGCACTTTGTGCTAGTC 780
QY	813	CTGSCACTGTGCACTCGCACTGGGCGAGTGTGCTGCTGCACCCATGGGCCCGCTGT 872
DB	781	CTGSCACTGTGCACTCGCACTGGGCGAGTGTGCTGCTGCACCCATGGGCCCGCTGT 840
QY	873	GCAGCTGGCTCATGCACTGTGTTCTACGTGCGGGCGGAGTGTCTCGTGCATGCTGCTG 932
DB	841	GCAGCTGGCTCATGCACTGTGTTCTACGTGCGGGCGGAGTGTCTCGTGCATGCTGCTG 900
QY	933	CGCCTCTTCTGGCCATGAGAGGGGAGCATATGAGTATGAATGCCCTCTACTTGGTA 992
DB	901	CGCCTCTTCTGGCCATGAGAGGGGAGCATATGAGTATGAATGCCCTCTACTTGGTA 960
QY	993	TATGTGCGCGTGTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 1052
DB	961	TATGTGCGCGTGTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 1020

QY	1053	GATGGGAATTGATGTTAGCGAGCCGTGTCAGGCGCCAGGTGTCACCCAACTACTTCTGG 1112
DB	1021	GATGGGAATTGATGTTAGCGAGCCGTGTCAGGCGCCAGGTGTCACCCAACTACTTCTGG 1080
QY	1113	ATGTCAGCGTTGCGTGGAGCCCCCGCCAGCTGGAAGCCCCCAGCAGATGCCACCGCA 1172
DB	1081	ATGTCAGCGTTGCGTGGAGCCCCCGCCAGCTGGAAGCCCCCAGCAGATGCCACCGCA 1140
QY	1173	GAAGAGCCCTTATGA 1187
DB	1141	GAAGAGCCCTTATGA 1155
RESULT 15		
AAI59336	standard; cDNA; 1438 BP.	
ID	AAI59336	
XX	AAI59336;	
AC	AAI59336;	
XX	22-OCT-2001 (first entry)	
DT	22-OCT-2001 (first entry)	
XX	Human polynucleotide SEQ ID NO 1539.	
DE	Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;	
XX	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukemia; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200153312-A1.	
PN	26-JUL-2001.	
XX	26-DEC-2000; 2000WO-US034263.	
XX	23-DEC-1999; 99US-00471275.	
PR	21-JAN-2000; 2000US-00488725.	
PR	25-APR-2000; 2000US-00552317.	
PR	20-JUN-2000; 2000US-00598042.	
PR	19-JUL-2000; 2000US-00620312.	
PR	03-AUG-2000; 2000US-00653450.	
PR	14-SEP-2000; 2000US-00682191.	
PR	19-OCT-2000; 2000US-00693036.	
PR	29-NOV-2000; 2000US-00727344.	
XX	(HYSE-) HYSEQ INC.	
PA	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
XX	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;	
PI	Zhou P, Goodrich R, Drmanac RT;	
PI	WPI: 2001-442253/47.	
XX	P-PSDB; AAM40180.	
DR	Novel nucleic acids and polypeptides, useful for treating disorders such	
XX	as central nervous system injuries.	
PT	Claim 1; SEQ ID NO 1539; 10078pp; English.	
XX	The invention relates to human nucleic acids (AAI57798-AAI61369) and the	
CC	encoded polypeptides (AAM38642-AAM42213) with nontropic,	
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localised neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilisation of the activities such as: Immune system suppression,	

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1438 BP; 251 A; 428 C; 463 G; 296 T; 0 U; 0 Other;

Query Match 95.1%; Score 1145.8; DB 4; Length 1438;
Best Local Similarity 99.4%; Pred. No. 8.2e-253;
Matches 1150; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db |||||
QY 1 ATGGATCCAGCGGGCGGCCCGCGGCGCTGCTCCCGCGCCCTGCGCGTGTGTGTGTG 60
Db |||||
QY 93 CTGAACCCCGCGCGGCGGCAAGGCGCTTTCAGAGCTTCTCCCGGAGTCACGTGCGAGCCC 152
Db |||||
QY 61 CTGAACCCCGCGCGGCGGCAAGGCGCTTTCAGAGCTTCTCCCGGAGTCACGTGCGAGCCC 120
Db |||||
QY 153 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGCGGAACACGCG 212
Db |||||
QY 121 CTTTGGCTGAGGCTGAATCTCTTCACGCTGATGCTCACTGAGCGGCGGAACACGCG 180
Db |||||
QY 213 CGGGAGCTGCTGCGGTCCGAGGAGCTGGGCGCTGGAGCGCTCTGGTGTATGCTGGA 272
Db |||||
QY 181 CGGGAGCTGCTGCGGTCCGAGGAGCTGGGCGCTGGAGCGCTCTGGTGTATGCTGGA 240
Db |||||
QY 273 GACGGGCTGATGACGAGGTGTTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCC 332
Db |||||
QY 241 GACGGGCTGATGACGAGGTGTTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCC 300
Db |||||
QY 333 ATCCAGAGCCCTGTGTAGCTCCGAGAGGCTCTGGCAACGCGCTCTGGCAACGCGCTTCCCTTG 392
Db |||||
QY 301 ATCCAGAGCCCTGTGTAGCTCCGAGAGGCTCTGGCAACGCGCTCTGGCAACGCGCTTCCCTTG 360
Db |||||
QY 393 AACCAATTATGCTGGCTATGAGCAGGTCAACCAATGAAGACCTCTGACCACTGACAGCTA 452
Db |||||
QY 361 AACCAATTATGCTGGCTATGAGCAGGTCAACCAATGAAGACCTCTGACCACTGACAGCTA 420
Db |||||
QY 453 TTGCTGTGCGCGGCTGTGTACCCATGAACCTGTCTCTGACACAGCGCTTCCGGGG 512
Db |||||
QY 421 TTGCTGTGCGCGGCTGTGTACCCATGAACCTGTCTCTGACACAGCGCTTCCGGGG 480
Db |||||
QY 513 CTGCGCTCTTCTCTGTGCTGAGCTGCGCTGGGCTTCAATGCTGATGGAACCTAGAG 572
Db |||||
QY 481 CTGCGCTCTTCTCTGTGCTGAGCTGCGCTGGGCTTCAATGCTGATGGAACCTAGAG 540
Db |||||
QY 573 AGTGAGAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCTGCGTCTG 632
Db |||||
QY 541 AGTGAGAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCTGCGTCTG 600
Db |||||
QY 633 GCAGCCTTTCGCACTTACCGCGCGGCTGAGCTTACCTCCCTGTAGGAAGAGTGGGTTCC 692
Db |||||
QY 601 GCAGCCTTTCGCACTTACCGCGCGGCTGAGCTTACCTCCCTGTAGGAAGAGTGGGTTCC 660
Db |||||
QY 693 AAGACACCTGCTCCCGCTTGTGTGTCAGAGGCGCGGTAGATGCAACCTTGTGCA 752
Db |||||
QY 661 AAGACACCTGCTCCCGCTTGTGTGTCAGAGGCGCGGTAGATGCAACCTTGTGCA 720
Db |||||
QY 753 CTGGAGGAGCAGTGCCTCTCACCTGAGCAGTGTGCGGAGGAGCTTTGTGCTAGTC 812
Db |||||
QY 721 CTGGAGGAGCAGTGCCTCTCACCTGAGCAGTGTGCGGAGGAGCTTTGTGCTAGTC 780
Db |||||
QY 813 CTGGCAGCTGCTGCACTCGCACCTGGGCGAGTGTGTTGTGTCACCCATGGGCGGCTGT 872
Db |||||
QY 781 CTGGCAGCTGCTGCACTCGCACCTGGGCGAGTGTGTTGTGTCACCCATGGGCGGCTGT 840
Db |||||
QY 873 GCAGCTGGGCTCATGATCTGTTCTACGTGCGGCGGAGTGTCTCGTGCCATGCTGCTG 932
Db |||||
QY 841 GCAGCTGGGCTCATGATCTGTTCTACGTGCGGCGGAGTGTCTCTGTCGATGCTGCTG 900
Db |||||
QY 933 CGCCTCTTCTGGCCATGGAGAGGCGGAGCATATGGAGTATGAATGCCCTTCTTGGTA 992
Db |||||

Db |||||
QY 901 CGCCTCTTCTGGCCATGGAGAGGCGAGCATATGAGTATGAATGCCCTTACTTGGTA 960
QY 993 TATGTGCCCGTGTGTCGCTTCCGCTTGGAGCCCAAGGATGGAAAGTATGTTTGGCAGTG 1052
Db |||||
QY 961 TATGTGCCCGTGTGTCGCTTCCGCTTGGAGCCCAAGGATGGAAAGTGTGTTTGGCAGTG 1020
QY 1053 GATGGGAAATTGATGTTAGGAGGCGCTGCGAGGCGGCGAGTGGACCCAAACTACTTCTGG 1112
Db |||||
QY 1021 GATGGGAAATTGATGTTAGGAGGCGCTGCGAGGCGGCGAGTGGACCCAAACTACTTCTGG 1080
QY 1113 ATGCTCAGCGGTTGCTGGAGCCCGCCCGCAGCTTGAAGCCCGCAGCAGATGCCACCGCCA 1172
Db |||||
QY 1081 ATGCTCAGCGGTTGCTGGAGCCCGCCCGCAGCTTGAAGCCCGCAGCAGATGCCACCGCCA 1140
QY 1173 GAAGAGCCCTTATGATC 1189
Db |||||
QY 1141 GAAGAGCCCTTATGACC 1157
Db |||||

Search completed: June 17, 2005, 03:59:30
Job time : 737 secs

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OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 03:27:54 ; Search time 4424 Seconds
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Title: US-10-642-289-1

Perfect score: 1205

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	839.4	69.7	1137	BM810136	BM810136 AGENCOURT
3	806.6	66.9	892	BI860351	BI860351 603387479
4	773	64.1	781	AY415128	AY415128 Homo sapi
5	739.8	61.4	1102	BX401290	BX401290 BX401290
6	725.2	60.2	785	BG680521	BG680521 602628344
7	715.2	59.4	888	BQ647377	BQ647377 AGENCOURT
8	708.8	58.8	1100	BM916526	BM916526 AGENCOURT
9	699.8	58.1	979	BX362837	BX362837 BX362837
10	694.6	57.6	963	BX363407	BX363407 BX363407
11	657.4	54.6	995	BX398860	BX398860 BX398860
12	625.6	51.9	633	CV027223	CV027223 5423 Full
13	622.6	51.7	793	BG678689	BG678689 602624488
14	614.4	51.0	875	BM006005	BM006005 603613736
15	606.4	50.3	671	AV694791	AV694791 AV694791
16	601.6	49.9	681	AY415129	AY415129 Pan trogl
17	594.8	49.3	952	BX362838	BX362838 BX362838
18	593.8	49.3	659	BE891653	BE891653 601434552
19	593.6	49.3	940	BQ626631	BQ626631 602293762
20	584.6	48.5	999	BQ675531	BQ675531 AGENCOURT
21	569.2	47.2	581	BP267514	BP267514 BP267514
22	567.6	47.1	798	CN156333	CN156333 943727 MA
23	526.2	43.7	842	BI648186	BI648186 603279314
24	520	43.2	569	CV028128	CV028128 6543 Full

25	513.8	42.6	1096	5	BX398861	BX398861
26	503.8	41.8	2145	3	BC011432	BC011432 Mus muscu
27	501.8	41.6	778	9	AY415130	AY415130 Mus muscu
28	501	41.6	4064	3	AK028667	AK028667 Mus muscu
29	500.2	41.5	944	5	BX363408	BX363408
30	495.8	41.1	941	6	CD518980	CD518980 AGENCOURT
31	480.6	39.9	947	4	BI415545	BI415545 602988310
32	475.2	39.4	1005	4	BM559257	BM559257 AGENCOURT
33	472.2	39.2	772	1	AI769914	AI769914 wj30d06.x
34	468.8	38.9	991	5	BUI58134	BUI58134 AGENCOURT
35	466.4	38.7	852	2	BE274434	BE274434 601120471
36	462.2	38.4	1075	4	BM557357	BM557357 AGENCOURT
37	460.8	38.2	478	2	BE740866	BE740866 601593092
38	457.8	38.0	763	6	CA307119	CA307119 UI-H-FTL-
39	457	37.9	624	7	CK969307	CK969307 4084694 B
40	456.6	37.9	809	4	BG280830	BG280830 602401209
41	439	36.4	603	2	BE275818	BE275818 601121616
42	410.8	34.1	710	6	CD366097	CD366097 UI-H-FTL-
43	407.8	33.8	700	5	BU626812	BU626812 UI-H-FLO-
44	406.8	33.8	705	5	BU630558	BU630558 UI-H-FLO-
45	394	32.7	618	2	AW916618	AW916618 EST347922

ALIGNMENTS

RESULT 1
BM808698
LOCUS BM808698 1054 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6582622 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471258
5', mRNA sequence.
ACCESSION BM808698
VERSION BM808698.1 GI:19125509
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1054)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/Drp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1979 row: 9 column: 03
High quality sequence start: 7
High quality sequence stop: 666.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5471258"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Db	1021	TTT 1023			
RESULT 2					
BM810136					
LOCUS	BM810136	1137 bp	mRNA	linear	EST 05-MAR-2002
DEFINITION	AGENCOURT_6579661 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5470089				
ACCESSION	BM810136				
VERSION	BM810136.1 GI:19126959				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1137)				
AUTHORS	NTH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1976 row: f column: 10 High quality sequence stop: 623.				
FEATURES	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:5470089"				
	/tissue_type="amelanotic melanoma, cell line"				
	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NIH MGC_41"				
	/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
ORIGIN					
Query Match		69.7%;	Score 839.4;	DB 4;	Length 1137;
Best Local Similarity		95.8%;	Pred. No. 4.7e-187;		
Matches 903;		Conservative 0;	Mismatches 32;	Indels 8;	Gaps 4;
QY	175	CCTTCACGCTGATGCTCACTGAGCGCGGAAACCAACGCGCGGAGCTGCTGCGGTGCGAGG	234		
DB	1	CCTTCACGCTGATGCTCACTGAGCGCGGAAACCAACGCGCGGAGCTGCTGCGGTGCGAGG	60		
QY	235	AGCTGGGCGCTGGGACGCTCTGGTGGTCACTGTCTGGAGACGGGCTCATGACGAGGTGG	294		
DB	61	AGCTGGGCGCTGGGACGCTCTGGTGGTCACTGTCTGGAGACGGGCTCATGACGAGGTGG	120		
QY	295	TGAACGGGCTCATGAGCGGCTGACTGGGAGACCGCCATCCAGAGCCCTGTGTAGCC	354		
DB	121	TGAACGGGCTCATGAGCGGCTGACTGGGAGACCGCCATCCAGAGCCCTGTGTAGCC	180		
QY	355	TCCACGAGCTCTGGCAACGGCTGGCAGCTTCCTTGAACCATTAATGCTGGCTATGAGC	414		
DB	181	TCCACGAGCTCTGGCAACGGCTGGCAGCTTCCTTGAACCATTAATGCTGGCTATGAGC	240		
QY	415	AGGTCAACAAATGAAGACCTCTGACCAACTGCACTATGCTGTGCGCGGCTGTGT	474		
DB	241	AGGTCAACAAATGAAGACCTCTGACCAACTGCACTATGCTGTGCGCGGCTGTGT	300		
QY	475	CACCCATGAACCTGCTGTCTGCACACGGCTTGGGGCTGGGCTCTTCTGTGTGCTCA	534		
DB	301	CACCCATGAACCTGCTGTCTGCACACGGCTTGGGGCTGGGCTCTTCTGTGTGCTCA	360		
QY	535	GCCTGGGCTGGGGCTTCATTGCTGATGTGGACTAGAGAGTGAGAGTATGGGCTCTGG	594		
DB	361	GCCTGGGCTGGGGCTTCATTGCTGATGTGGACTAGAGAGTGAGAGTATGGGCTCTGG	420		
QY	595	GGGAGATGCGCTTCACTCTGGGCACTTTCTGCGCTTGGCAGCCTTGGCCTTACCGCG	654		
DB	421	GGGAGATGCGCTTCACTCTGGGCACTTTCTGCGCTTGGCAGCCTTGGCCTTACCGCG	480		
QY	655	GCCGACTGGCTTACCTCCCTGTAGAGAGTGGGTTCAGACACACTGCTCCCGCTTG	714		
DB	481	GCCGACTGGCTTACCTCCCTGTAGAGAGTGGGTTCAGACACACTGCTCCCGCTTG	540		
QY	715	TGCTCCAGCAGGCGCGGTAGATGACACACTTGTGCCACTGGAGGAGCAGTGCCCTCTC	774		
DB	541	TGCTCCAGCAGGCGCGGTAGATGACACACTTGTGCCACTGGAGGAGCAGTGCCCTCTC	600		
QY	775	ACTGGACAGTGTGTCGCGACGAGGACTTTGTGTAGTCTCTGGCACTGCTGCACCTCG	834		
DB	601	ACTGGACAGTGTGTCGCGCGACGAGGACTTTGTGTAGTCTCTGGCACTGCTGCACCTCG	660		
QY	835	TGGGACGATGAGATGTTTGTCTGCACCCATGGGCGCTGTGACGCTGGCGTCAATGATCTGT	894		
DB	661	TGGGACGATGAGATGTTTGTCTGCACCCATGGGCGCTGTGACGCTGGCGTCAATGATCTGT	720		
QY	895	TCTACGTGC - GGGCGGAGTGTCTGTCGCCATGCTGCTGCGCCTCTTCTGGCCATGAG	953		
DB	721	TCTACGTGCGGGCGGAGTGTCTGTCGCCATGCTGCTGCGCCTCTTCTGGCCATGAG	780		
QY	954	AAGGCGAGGCTATGAGATGAATGCCCTACTTTGGTATATGTGCGCGTGTGCGCTTC	1013		
DB	781	AAGGCGAGGCTATGAGATGAATGCCCTACTTTGGGATATGTGCGCGTGTGCGCTTC	840		
QY	1014	CGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA - -TGGGGAATTGATGTTA	1071		
DB	841	CGCTTGGAGCCCAAGGATGGGAAAGTATGTTTGCAGTGA - -TGGGGAATTGATGTTA	900		
QY	1072	GC - -GAGGCGCTGACGGCCAGGTGCACCCAACTACTTCTGGATGGTC - - - -AGCGGTT	1125		
DB	901	GCCGAGGCGCGTGCAGGGGCGAGTGCACCCAACTATTATTTTGGAGAGGGGCCCAAGGGGTG	960		
QY	1126	CGCTGGAGCCCCCGCC - -AGCTGGAAGCCCCAGCAGATG - -CCACCGCCAGAGAGCCCT	1182		
DB	961	GGGTGGAGCCCCCCCCCAGCTGGAAACCCCCCGCAGATGCCCCACCGCCAAAGAGCCC	1020		
QY	1183	TAT 1185			

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	ORIGIN	
	Query Match	66.9%; Score 806.6; DB 4; Length 892;
	Best Local Similarity	96.8%; Pred. No. 2.5e-179;
	Matches	866; Conservative 0; Mismatches 24; Indels 5; Gaps 4;
QY	286	ACGAGGTGGTGAAACCGGCTCATGAGCGGCTGACTGGGAGACGCCATCCAGAAGCCCC 345
DB	1	ACGAGGTGGTGAAACCGGCTCATGAGCGGCTGACTGGGAGACGCCATCCAGAAGCCCC 60
QY	346	TGTGTAGCCTCCAGCAGGCTTCGGCAACGGCTGGCAGCTTCCTTTGAACATTATGCTG 405
DB	61	TGTGTAGCCTCCAGCAGGCTTCGGCAACGGCTGGCAGCTTCCTTTGAACATTATGCTG 120
QY	406	GCTATGACAGCTCACCAATGAAGACCTCTCTGACCAACTGACGCTATTGCTGTGGCGC 465
DB	121	GCTATGACAGCTCACCAATGAAGACCTCTCTGACCAACTGACGCTATTGCTGTGGCGC 180
QY	466	GGCTGCTCTCAACCANTGAACCTGTGCTCTGTCACACGGCTTCGGGGCTCGGCTCTTCT 525
DB	181	GGCTGCTCTCAACCANTGAACCTGTGCTCTGTCACACGGCTTCGGGGCTCGGCTCTTCT 240
QY	526	CTGTGCTCAGCTGGCTGGGGCTTCATGCTGATGTGGACCTTAGAGAGTGAGAAGTATC 585
DB	241	CTGTGCTCAGCTGGCTGGGGCTTCATGCTGATGTGGACCTTAGAGAGTGAGAAGTATC 300
QY	586	GGCGTCTGGGGAGATGGCTTCACTCTGGGCACTTTCTCGCTCTGGCAGCTTGGCGCA 645
DB	301	GGCGTCTGGGGAGATGGCTTCACTCTGGGCACTTTCTCGCTCTGGCAGCTTGGCGCA 360
QY	646	CTTACCGCGCGCACTGGCTTACCTCCCTGTAGGAAGTGGGTTCGAAGACACCTCGCT 705
DB	361	CCTACCGCGCGCACTGGCTTACCTCCCTGTAGGAAGTGGGTTCGAAGACACCTCGCT 420
QY	706	CCCCGTTGTGTTCAGCAGGCGCGGTAGATGACACCTTGTGCCACTCGAGGAGCCAG 765
DB	421	CCCCGTTGTGTTCAGCAGGCGCGGTAGATGACACCTTGTGCCACTCGAGGAGCCAG 480
QY	766	TGCCCTCTCACTGGACAGTGGTGGCCGACGAGGACTTTGTCTAGTCTGTGCACTGTGTC 825
DB	481	TGCCCTCTCACTGGACAGTGGTGGCCGACGAGGACTTTGTCTAGTCTGTGCACTGTGTC 540
QY	826	ACTCGCACCTGGGCACTGAGATGTTTGTGCAACCCATGGGCGCTGTGACGCTGGCGTCA 885
DB	541	ACTCGCACCTGGGCACTGAGATGTTTGTGCAACCCATGGGCGCTGTGACGCTGGCGTCA 599
QY	886	TGCACTGTGTTACGTGGGGGGGAGTGTCTGTGCACTGCTGCTGGCTCTTCTCTGG 945
DB	600	TGCACTGTGTTACGTGGGGGGGAGTGTCTGTGCACTGCTGCTGGCTCTTCTCTGG 659
QY	946	CCATGGAGAAGGCGAGGCATATGAGTAAATGATGATGATGATGATGATGATGATGATG 1005
DB	660	ACATGGAGAAGGCGAGGCATATGAGTAAATGATGATGATGATGATGATGATGATGATG 719
QY	1006	TGCGCTTTCGCTTGGAGCCCAGAGTATG-TGGAAAGTATGTTTGGAGTGGATGGGAATG 1064
DB	720	TGCGCTTTCGCTTGGAGCCCAGAGTATG-TGGAAAGTATGTTTGGAGTGGATGGGAATG 779
QY	1065	ATGGTTAGCGAGGCGGTGACGGGCCAGGTGACCCAACTACTTCTTGATGTTGTCAGCGGT 1124

||||| 780 ATGGTTAGGAGCGGTGAGGCGCCAGGTGACGCCAAA-TACTTCTGGATGGTCAGCGGT 838
||||| 1125 TGCCTGGAGCCCCCAGCTGGGAAGCCCCAGCAGATGCCACCGCCAGAAAGAGC 1179
||||| 839 TGC--TGGAGCCCCCGCCAGCTGGGAAGCCCCAGCAGATGCCACCGCAGAAAAGC 891

Db

QY

Db

RESULT 4
AY415128 781 bp DNA linear GSS 17-DEC-2003
LOCUS Homo sapiens SPHK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY415128
VERSION AY415128.1 GI:39771087
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 781)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 781)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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gene

ORIGIN

Query Match 64.1%; Score 773; DB 9; Length 781;
Best Local Similarity 99.4%; Pident.No. 2e-171;
Matches 776; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 407 CTATGAGCAGGTTCACCAATGAAGACCTCTCAGCAACATGACGCTATTGCTGTGCGCGCG 466
||||| 1 CTATGAGCAGGTTCACCAATGAAGACCTCTCAGCAACATGACGCTATTGCTGTGCGCGCG 60
||||| 467 GCTGCTGTACCCATGAACCTGCTCTCTGTCACACGCTTCGGGGCTGCGCCTCTTCTC 526
||||| 61 GCTGCTGTACCCATGAACCTGCTCTCTGTCACACGCTTCGGGGCTGCGCCTCTTCTC 120
||||| 527 TGTGCTCAGCTGGCGCTGCGGCTTCATGCTGATGTGGACCTAGAGAGTGAGAGTATCG 586
||||| 121 TGTGCTCAGCTGGCGCTGCGGCTTCATGCTGATGTGGACCTAGAGAGTGAGAGTATCG 180
||||| 587 GCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCTCGCTCTGGCAGCGCTTGGCGCAC 646
||||| 181 GCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCTCGCTCTGGCAGCGCTTGGCGCAC 240
||||| 647 TTACCGCGCGCAGATGCGCTTACCTCCCTGTAGGAAGAGTGCGGTTCGAAGACACCTGCGCTC 706
||||| 241 CTACCGCGCGCAGATGCGCTTACCTCCCTGTAGGAAGAGTGCGGTTCGAAGACACCTGCGCTC 300

QY 707 CCCCGTTGTTGGTCCAGCAGGGCCCGGTAGATGCACACTTGTGCGCACTGGAGGAGCCAGT 766
||||| 301 CCCCGTTGTTGGTCCAGCAGGGCCCGGTAGATGCACACTTGTGCGCACTGGAGGAGCCAGT 360
||||| 767 GCCCTCTCACTGGACAGTGGTGGCCGACGAGGACTTTGTGTAGTCTCTGACACTGTGCTGCA 826
||||| 361 GCCCTCTCACTGGACAGTGGTGGCCGACGAGGACTTTGTGTAGTCTCTGACACTGTGCTGCA 420
||||| 827 CTGCACTCTGGGCGAGTGAATGTTTGTGTCACCCATGGGCGGCTGTGCAGCTGGCGTCAT 886
||||| 421 CTGCACTCTGGGCGAGTGAATGTTTGTGTCACCCATGGGCGGCTGTGCAGCTGGCGTCAT 480
||||| 887 GCATCTCTTACGTGCGGGCGGAGTGTCTCGTGCCATGCTGTCGCGCTCTTCTGCGGC 946
||||| 481 GCATCTCTTACGTGCGGGCGGAGTGTCTCGTGCCATGCTGTCGCGCTCTTCTGCGGC 540
||||| 947 CATGGAGAAGGCGGACGATATGAGTATGAATGCCCTACTTGGTATATGTGCCCGTGGT 1006
||||| 541 CATGGAGAAGGCGGACGATATGAGTATGAATGCCCTACTTGGTATATGTGCCCGTGGT 600
||||| 1007 GCGCTTCCGCTTGGAGCCCAAGGATGGAAAGTATGTTTGCAGTGATGGGGAATTGAT 1066
||||| 601 GCGCTTCCGCTTGGAGCCCAAGGATGGAAAGTGTGTTTGCAGTGATGGGGAATTGAT 660
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||||| 661 GGTTAGCGAGGCGCTGCGAGGCGCCAGGTGCACCAAACTACTTCTGGATGGTCAGCGGTG 720
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QY 1187 A 1187
Db 781 A 781

RESULT 5
BX401290 1102 bp mRNA linear EST 29-APR-2004
LOCUS BX401290 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DK011YD19 3-PRIME, mRNA sequence.
ACCESSION BX401290
VERSION BX401290.2 GI:46877697
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30626413.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1102
/organism="Homo sapiens"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.

ORIGIN	Query Match Best Local Similarity Matches 789; Conservative 1; Mismatches 8; Indels 5; Gaps 4;
QY	387 TCCTTGAACCATATATGCTGGCTATGAGCAGGTTCACATGAAGACTCTCTGACCAACTGC 446
Db	1033 TCCTTGAACCATATATGCT-GCTATGAGCA-GTCACCAATGAAGACTCTCTGACCAACTGC 976
QY	447 AGCTATTGCTGTGGCGCGGTCTGTACCCATGAACCTGCTCTCTGACACAGCT 506
Db	975 AGCTATTGCTGTGGCGCGGTCTGTACCCATGAACCTGCTCTCTGACACAGCT 916
QY	507 TCGGGCTGCGCTCTTCTCTGTGCTCAGCTGGCTGGGGCTTCATTGCTGATGGAC 566
Db	915 TCGGGG--GCGGCTCTTCTGTGCTCAGCTGGCTGGGGCTTCATTGCTGATGGAC 858
QY	567 CTAGAGAGTGAGAAGTATCGGCTCTGGGGAGATGCGCTTCATCTGGGCACTTTCCTG 626
Db	857 CTAGAGAGTGAGAAGTATCGGCTCTGGGGAGATGCGCTTCATCTGGGCACTTTCCTG 798
QY	627 CGTCTGGAGCTTGGGCACTTACCGCGCGCACTGGCTTACCTCCCTGTAGGAAGAGTG 686
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QY	687 GGTTCACAGACACTGCTCCCTCCCGTTGTGTCACAGCGGCGCGGTAGATGACACACTT 746
Db	737 GGTTCACAGACACTGCTCCCTCCCGTTGTGTCACAGCGGCGCGGTAGATGACACACTT 678
QY	747 GTGCCACTGGAGAGCAGTGGCTCTCACTGACAGTGGTCCGACGAGACTTTTGTG 806
Db	677 GTGCCACTGGAGAGCAGTGGCTCTCACTGACAGTGGTCCGACGAGACTTTTGTG 618
QY	807 CTAGTCTGGCACTGTGCACTGCACTGGGCACTGAGATGTTTCTGCACCCATGGGC 866
Db	617 CTAGTCTGGCACTGTGCACTGCACTGGGCACTGAGATGTTTCTGCACCCATGGGC 558
QY	867 CGCTGTGAGCTGGCGTCAATGATCTTCTAGTGGCGGCGGAGTGTCTCGTGCCATG 926
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QY	927 CTGCTGGCGCTCTTCTTGGCCATGAGAGAGGCGAGGCATATGAGTATGAATGCCCTTAC 986
Db	497 CT-CTGGCGCTCTTCTTGGCCATGAGAGAGGCGAGGCATATGAGTATGAATGCCCTTAC 439
QY	987 TTGGTATATGCGCGTGTGCGCTTCCGCTTGGAGCCCAAGATGGGAAAGTATGTTT 1046
Db	438 TTGGTATATGCGCGTGTGCGCTTCCGCTTGGAGCCCAAGATGGGAAAGTATGTTT 379
QY	1047 GCAGTGGATGGGAATGATGTTTACGAGCGCTGTCAGGCGCGTGCAGGCGCAGTGCACCCAACTAC 1106
Db	378 GCAGTGGATGGGAATGATGTTTACGAGCGCTGTCAGGCGCGTGCAGGCGCAGTGCACCCAACTAC 319
QY	1107 TTCTGATGTCAGCGGTTTCGCTGGAGAGCCCGCCAGCTGGAGAGCCCGCAGAGATGCCA 1166
Db	318 TTCTGATGTCAGCGGTTTCGCTGGAGAGCCCGCCAGCTGGAGAGCCCGCAGAGATGCCA 259
QY	1167 CCGCAGAAAGAGCCCTTATGATC 1189
Db	258 CCGCAGAAAGAGCCCTTATGATC 236

RESULT 6
BG680521
LOCUS
DEFINITION 602628344F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753187 5',
mRNA sequence.
ACCESSION BG680521
VERSION BG680521.1 GI:13911918

KEYWORDS

EST.
Homo sapiens (human)

SOURCE

ORGANISM
Homo sapiens

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 785)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10612 row: g column: 12

High quality sequence stop: 783.

Location/Qualifiers

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/db_xref="taxon:9606"

/clone="IMAGE:4753187"

/tissue_type="squamous cell carcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI CGAP_Skn4"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI CGAP Library."

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Technologies. Note: this is a NCI CGAP Library."

Technologies. Note: this is a NCI CGAP Library."

Db	481	TCATGCATCTGTTCTACGTGGCGGGAGTGTCGTGTGCATGCTGCTGGCGCTCTTTC	540
Qy	943	TGGCCATGGAGAGCGGAGGCATATGAGTATGAATGCAATGCCCCCTACTTGGTATATGTGCCCC	1002
Db	541	TGGCCATGGAGAGCGGAGGCATATGAGTATGAATGCCCCCTACTTGGTATATGTGCCCC	600
Qy	1003	TGTCGGCTTCCCG-TTTGGAGCCCAAGATGGGAAAGGTATGTTTTCAGTGGATGGGAA	1061
Db	601	TGTCGGCTTCCCGTTTGGAGCCCAAGATGGGAAAGGTGTTTTCAGTGGATGGGAA	660
Qy	1062	TTGATGTTACGAGGCGCGTCAGGGCCAGGTGCACCAACTACTTCTCGATGGTTCAGC	1121
Db	661	TTGATGTTACGAGGCGCGTCAGGGCCAGGTGCACCAACTACTTCTCGATGGTTCAGC	718
Qy	1122	GTTTGGCTGGAGCCCCCGCCCGCAGCTGGAAGCCCCCAGCAGATGCCACCGCAGAAAGAGCCC	1181
Db	719	GTTTGGCTGGAGCCCCCG-CCAGCTGGAAGCCCCCAGCAGATGCCACCG-CAGAGAGGCC	776
Qy	1182	TTATGATC 1189	
Db	777	TTATGACC 784	
RESULT 7			
LOCUS	B0647377		
DEFINITION	AGENCOURT 8414975 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6272071	888 bp mRNA linear EST 15-JUL-2002	
ACCESSION	B0647377		
VERSION	B0647377.1	GI:21771549	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 888)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: csapbs@email.nih.gov Tissue Procurement: CGAP (Stanford) cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHC2449 row: n column: 08 High quality sequence start: 6 High quality sequence stop: 668.		
FEATURES			
source	1..888		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6272071"		
	/tissue_type="hepatocellular carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_100"		
	/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	59.4%	Score 715.2; DB 5; Length 888;	
Best Local Similarity	98.7%	Pred. No. 8.7e-158;	

Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCW2009 row: n column: 15
 High quality sequence stop: 625.
 Location/Qualifiers
 1. 1100
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5482958"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 41"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 58.8%; Score 708.8; DB 5; Length 1100;
 Best Local Similarity 89.3%; Pred. No. 2.9e-156;
 Matches 843; Conservative 0; Mismatches 80; Indels 21; Gaps 7;

QY 175 CTTTACGCTGATGCTCACTGAGCGCGGAACACGCGGGAGCTGTGGGTGGAGG 234
 DB 1 CTTTACGCTGATGCTCACTGAGCGCGGAACACGCGGGAGCTGTGGGTGGAGG 60

QY 235 AGCTGGGCGCTGGAGCGCTCTGTGCTCATGCTGGAGACGGCTGTGACGAGGTGG 294
 DB 61 AGCTGGGCGCTGGAGCGCTCTGTGCTCATGCTGGAGACGGCTGTGACGAGGTGG 120

QY 295 TGAACGGGCTCATGAGCGCGCTGACTGGAGACCGCCATCCAGAACGCCCTGTGTAGCC 354
 DB 121 TGAACGGGCTCATGAGCGCGCTGACTGGAGACCGCCATCCAGAACGCCCTGTGTAGCC 180

QY 355 TCCAGCAGGCTCTGGCAACGCGCTGGAGCTTCTTGTGAACATTATGCTGGCTATGACG 414
 DB 181 TCCAGCAGGCTCTGGCAACGCGCTGGAGCTTCTTGTGAACATTATGCTGGCTATGACG 240

QY 415 AGGTACCAATGAGACCTCTGACCAACTGACGCTATTGCTGTGCGCGCGCTGCTGT 474
 DB 241 AGGTACCAATGAGACCTCTGACCAACTGACGCTATTGCTGTGCGCGCGCTGCTGT 300

QY 475 CACCCATGAACCTGTGCTCTGCACACGGCTTTCGGGGCTGCGCCTCTTCTGTGCTCA 534
 DB 301 CACCCATGAACCTGTGCTCTGCACACGGCTTTCGGGGCTGCGCCTCTTCTGTGCTCA 360

QY 535 GCCTGGCTGGGGCTTCATTGCTGATGTGACCTAGAGAGTGAGAGTATGCGCGTCTGG 594
 DB 361 GCCTGGCTGGGGCTTCATTGCTGATGTGACCTAGAGAGTGAGAGTATGCGCGTCTGG 420

QY 595 GGAGATGCGCTTCACTCTGGGCACTTCTGCTGCTGGGAGCTTGGGAGCTTACGCGG 654
 DB 421 GGAGATGCGCTTCACTCTGGGCACTTCTGCTGCTGGGAGCTTGGGAGCTTACGCGG 480

QY 655 GCGGACTGGCTTACCTCCCTGTAGGAGAGTGAGGTTCCAGACACCTGCTCCCGGTTG 714
 DB 481 GCGGACTGGCTTACCTCCCTGTAGGAGAGTGAGGTTCCAGACACCTGCTCCCGGTTG 540

QY 715 TGTTCAGCAGGGGCGCGGTAGATGACACCTTGTGACCTGGAGGAGCAGTCCCTCTC 774
 DB 541 TGTTCAGCAGGGGCGCGGTAGATGACACCTTGTGACCTGGAGGAGCAGTCCCTCTC 600

QY 775 ACTGGACAGTGGTGCCCGACGAGGACTTTGTGTAGTCTGTGGGACGTGCTGCATCGCAC 834

DB 601 ACTGGACAGTGGTGGCCGACGAGGACTTTGTGCTAGTCTGGCACTGCTGCACCTGCACC 660
 QY 835 TGGGC--AGTCAGATGTTTGTGTCACCATCGGC--CGCTGTCAGCTGGCGTTCATGCATC 891
 DB 661 TGGGNCAGNTAGATGTTTGTGTCACCATGCGGCTGTGTCAGCTGGCGTTCATGCATC 720
 QY 892 TGTTCACGTGCGGCGG-----GAGTGTCTCGTGGCATGCTGCTGGCGCTCTTCCTGG 945
 DB 721 TGTTCACGNCNNGNGCGGGAAGTGTCTCGTGCCATGCTGCTGGCGCTCTTCCTG 780
 QY 946 CCAT--GGAGAGGCGCAGCATATGGAG----TATGATGCCCTTACTTGTATAT--GT 997
 DB 781 NCCTTGGAAAAAGGCGAGGCCATTGTTGGGAAGTAATGATGGCCCTTAACCTGGGATATGG 840
 QY 998 GCCGTGCTGCTTCCCTTCCGCTTGGAGCCCAAGG----ATGGGAAGGATATGTTTTCAGTGG 1053
 DB 841 GCCGTGCGGCCCTTCCCTTGGAAACCCAGGGATGTTGGAAAAAGGCTGTTTTCAGGG 900
 QY 1054 ATGGGGAATTGATGTTAGCGAGGCGCTGTCAGGGCCAGGTGCAC 1097
 DB 901 AATGGGGAATTGATGTTTACCCAGCCCGCCAGGGCCC 944

RESULT 9
 BX362837/c 979 bp mRNA linear EST 05-MAY-2003
 LOCUS BX362837 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DK004YP21 3-PRIME, mRNA sequence.
 ACCESSION BX362837
 VERSION BX362837.1 GI:30370643
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 979)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK004CH1NP1.
 FEATURES
 Location/Qualifiers
 1. 979
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK004YP21"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 58.1%; Score 699.8; DB 5; Length 979;
 Best Local Similarity 98.3%; Pred. No. 3.8e-154;
 Matches 734; Conservative 4; Mismatches 6; Indels 3; Gaps 3;

QY 443 CTGACGCTATTGCTGTGCGCGGCTGTGTCACCCATGAACTGCTGTCTGCACAC 502
 DB 979 CTGACGCTATTGCTGTGTS-CSCCGGCTGTGTCACCCATGAACTGCTGTCTGCACAC 921
 QY 503 GGTTCGGGGCTGCGCTCTTCTGCTGCTGAGCTGGGCTTCATTGCTGATGT 562

Db 920 GGCCTTCGGGG-TGCGCCTCTTCTGTGTCTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGT 862
QY 563 GGACCTAGAGAGTGAGAGATATGCGCGTCTGGGGAGATGCGCTTCACTCTGGGCACTTT 622
Db 861 GGACCTAGAGAGTGAGAGATATGCGCGTCTGGGGAGATGCGCTTCACTCTGGGCACTTT 802
QY 623 CTTGGCTTGGCAGCCTTGGCGACTTACGGCGCCGACTGGCTTACCTCCCTGTAGGAAG 682
Db 801 CTTGGCTTGGCAGCCTTGGCGACTTACGGCGCCGACTGGCTTACCTCCCTGTAGGAAG 742
QY 683 AGTGGGTTCCAAAGACACCTGCTCCCGCTTGTGTCTCAGCAGGGCCCGGTAGATGACA 742
Db 741 AGTGGGTTCCAAAGACACCTGCTCCCGCTTGTGTCTCAGCAGGGCCCGGTAGATGACA 682
QY 743 CTTGTGCTCAGTGGAGGAGCCAGTCCCTCTCACTGGACAGTGTGCGCGACGAGACTT 802
Db 681 CTTGTGCTCAGTGGAGGAGCCAGTCCCTCTCACTGGACAGTGTGCGCGACGAGACTT 622
QY 803 TGTGTAGTCTGGCAGCTGCTGCACTCGCACCTGGGCGAGTGAGATGTTTGTGCACTCCAT 862
Db 621 TGTGTAGTCTGGCAGCTGCTGMACTCGCACCTGGGCGAGTGAGATGTTTGTGCACTCCAT 562
QY 863 GGGCGCTGTGCGAGCTGGCGTCACTGATCATCTGTTCTACGTGGGGCGGAGTGTCTCGTGC 922
Db 561 GGGCGCTGTGCGAGTGGCGTCACTGATCATCTGTTCTACGTGGGGCGGAGTGTCTCGTGC 502
QY 923 CATGCTGTGCGCCTCTTCTGGCCATGGAGAGGCGAGGCATATGGAGTATGAATGCC 982
Db 501 CATGCT-CTGCGCCTCTTCTGGCCATGGAGAGGCGAGGCATATGGAGTATGAATGCC 443
QY 983 CTACTTGTATATGTGCGCGTGTGCTTCCGCTTGGAGCCCAAGATGGAGAAAGTAT 1042
Db 442 CTACTTGTATATGTGCGCGTGTGCTTCCGCTTGGAGCCCAAGATGGAGAAAGTGT 383
QY 1043 GTTTCAGTGGATGGGAAATGATGGTTAGCGAGCGCTGCGAGGCGCAGGTGCACCCAAA 1102
Db 382 GTTTCAGTGGATGGGAAATGATGGTTAGCGAGCGCTGCGAGGCGCAGGTGCACCCAAA 323
QY 1103 CTACTTGTGATGTGACGGTGTGCTGGAGCCCGCCCGCCAGCTGGAGCCCGACAGAT 1162
Db 322 CTACTTGTGATGTGACGGTGTGCTGGAGCCCGCCCGCCAGCTGGAGCCCGACAGAT 263
QY 1163 GCCACCGCAGAGAGCCCTTATGATC 1189
Db 262 GCCACCGCAGAGAGCCCTTATGACC 236

RESULT 10
BX363407/c
LOCUS BX363407 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK012YL15 3-PRIME, mRNA sequence.
ACCESSION BX363407
VERSION BX363407.2 GI:46550533
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 963)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378729.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK012YL15"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/primer="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 57.6%; Score 694.6; DB 5; Length 963;
Best Local Similarity 98.6%; Pred. No. 6.4e-153;
Matches 719; Conservative 2; Mismatches 6; Indels 2; Gaps 2;
QY 461 CCGCGCGCTGTGTACCCATGAACCTGTCTCTCTGCAACAGGCTTCGGGGCTGCGCCT 520
Db 954 SCGCCGCTGTGTACCCATGAACCTGTCTCTCTGCAACAGGCTTCGGGG-TCGCGCT 896
QY 521 CTTCTCTGTGTCAAGCCTGGCGCTTCAATGCTGATGTGACCTAGAGAGTGAGAA 580
Db 895 CTTCTCTGTGTCAAGCCTGGCGCTTCAATGCTGATGTGACCTAGAGAGTGAGAA 836
QY 581 GTATCGCGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTTCCTGCGTCTGGCAGCCTT 640
Db 835 GTATCGCGCTGTGGGGAGATGCGCTTCACTCTGGGCACTTTCCTGCGTCTGGCAGCCTT 776
QY 641 GCGCACTTACCGCGCGCAGCTGGCTTACCTCCCTGTAGGAAGTGGGTTCGAAGACACC 700
Db 775 GCGCACTTACCGCGCGCAGCTGGCTTACCTCCCTGTAGGAAGTGGGTTCGAAGACACC 716
QY 701 TGCTCTCCCGTGTGTGTCAGCAGGCGCGGTAGATGCACCTTGTGCCACTGGAGGA 760
Db 715 TGCTCTCCCGTGTGTGTCAGCAGGCGCGGTAGATGCACCTTGTGCCACTGGAGGA 656
QY 761 GCCAGTCCCTCTCACTGGACAGTGTGTCGCCAGCAGGACTTTGTGCTAGTCTTGGCACT 820
Db 655 GCCAGTCCCTCTCACTGGACAGTGTGTCGCCAGCAGGACTTTGTGCTAGTCTTGGCACT 596
QY 821 GCTGCACTCGCACTCGGCGAGTGGATGTTTGTGTCACCCATGGCGCGCTGTGCACTGG 880
Db 595 GCTGCACTCGCACTCGGCGAGTGGATGTTTGTGTCACCCATGGCGCGCTGTGCACTGG 536
QY 881 CGTCATGCATCTGTTCTACGTGGCGCGGAGTGTCTCGTGCCATGTGCTGCGCCTCTT 940
Db 535 CGTCATGCATCTGTTCTACGTGGCGCGGAGTGTCTCGTGCCATGTCT-STGCCCTCTT 477
QY 941 CTTGGCCATGGAGAAAGGCGCAGCATATGGAGTATGAATGCCCTTACTTGGTATATGTGCC 1000
Db 476 CTTGGCCATGGAGAAAGGCGCAGCATATGGAGTATGAATGCCCTTACTTGGTATATGTGCC 417
QY 1001 CGTGGTCCCTTCTGCTTGGAGCCCAAGGATGGAAAGGTATGTTTGCAGTGGATGGGA 1060
Db 416 CGTGGTCCCTTCTGCTTGGAGCCCAAGGATGGAAAGGTGTGTTTGCAGTGGATGGGA 357
QY 1061 ATTGATGTTAGCGAGCGCTGCGAGGCGCAGGTGACCCAACTACTTCTGGAATGTGAG 1120
Db 356 ATTGATGTTAGCGAGCGCTGCGAGGCGCAGGTGACCCAACTACTTCTGGAATGTGAG 297
QY 1121 CGGTTGCGTGGAGCCCGCCGCTGGAAGCCCGCAGAGATGCCAGCCGACAGAGACC 1180
Db 296 CGGTTGCGTGGAGCCCGCCGCTGGAAGCCCGCAGAGATGCCAGCCGACAGAGACC 237
QY 1181 CTTATGATC 1189
Db 236 CTTATGACC 228

RESULT 11

Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN	Query Match	51.9%;	Score 625.6;	DB 7;	Length 633;
	Best Local Similarity	99.4%;	Pred. No. 1.1e-136;		
	Matches 628;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	33	ATGGATCCAGCGCGCGCCCGCGGCGTGTCTCCCGCGGCGCTGCGGCGTGTGTGTGTG 92			
DB	1	ATGGATCCAGCGCGCGCCCGCGGCGTGTCTCCCGCGGCGCTGCGGCGTGTGTGTG 60			
QY	93	CTGAACCCGCGCGCGCGCAAGGCGAAGGCTTGGAGCTTCTCCGGAGTCACTGTCAGGCC 152			
DB	61	CTGAACCCGCGCGCGCGCAAGGCGAAGGCTTGGAGCTTCTCCGGAGTCACTGTCAGGCC 120			
QY	153	CTTTTGGCTGAGGCTGAATCTCTTCAAGCTGTGCTCACTGAGCGCGGAACACACGCG 212			
DB	121	CTTTTGGCTGAGGCTGAATCTCTTCAAGCTGTGCTCACTGAGCGCGGAACACACGCG 180			
QY	213	CGGAGCTGGTGCCTGCGAGAGCTGGGCGCGTCTGGGACGCTCTGGTGTCTATGTCTGGA 272			
DB	181	CGGAGCTGGTGCCTGCGAGAGCTGGGCGCGTCTGGGACGCTCTGGTGTCTATGTCTGGA 240			
QY	273	GACGGCTGTATGACAGAGTGTGAACGGGCTATGAGAGCGGCTGACTGGGAGACCGCC 332			
DB	241	GACGGGCTGTATGACAGAGTGTGAACGGGCTATGAGAGCGGCTGACTGGGAGACCGCC 300			
QY	333	ATCCAGAAGCCCTGTGTAGCTCCACGAGCTCTGGCAACGGCTGGGAGCTTCTCTTG 392			
DB	301	ATCCAGAAGCCCTGTGTAGCTCCACGAGCTCTGGCAACGGCTGGGAGCTTCTCTTG 360			
QY	393	AACCAATTATGTGGCTATGACAGGTCAACCAATGAAGACCTCTGACCAACTGACCGCTA 452			
DB	361	AACCAATTATGTGGCTATGACAGGTCAACCAATGAAGACCTCTGACCAACTGACCGCTA 420			
QY	453	TGCTGTGCGCGCGCTGCTACCCATGAACCTGTCTCTGCAACCGGCTTGGGG 512			
DB	421	TGCTGTGCGCGCGCTGCTACCCATGAACCTGTCTCTGCAACCGGCTTGGGG 480			
QY	513	CTGCGCTCTTCTGTCTGTCTGTGCTGTGGGCTTCAATGCTGATGTGACCTAGAG 572			
DB	481	CTGCGCTCTTCTGTCTGTCTGTGCTGTGGGCTTCAATGCTGATGTGACCTAGAG 540			
QY	573	AGTGAGAAGTATCGCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTGCGTCTG 632			
DB	541	AGTGAGAAGTATCGCGCTCTGGGGAGATGCGCTTCACTCTGGGCACTTTCTGCTTCTG 600			
QY	633	CGAGCCTTGGGCACTTACCGGCGGCGACTGGC 664			
DB	601	CGAGCCTTGGGCACTTACCGGCGGCGACTGGC 632			

RESULT 13
BG678689
LOCUS 602624488F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749573 5',
DEFINITION mRNA sequence.
ACCESSION BG678689
VERSION BG678689.1 GI:13910086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10602 row: p column: 22
High quality sequence stop: 669.

FEATURES
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1..793
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4749573"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN	Query Match	51.7%;	Score 622.6;	DB 4;	Length 793;
	Best Local Similarity	93.3%;	Pred. No. 5.9e-136;		
	Matches 740;	Conservative 0;	Mismatches 39;	Indels 14;	Gaps 8;
QY	173	CTCCTTTCACGCTGATGCTCACTGAGCGCGGGAACACGCGCGGAGCTGTGCGGTCCGA 232			
DB	1	CTCCTTTCACGCTGATGCTCACTGAGCGCGGGAACACGCGCGGAGCTGTGCGGTCCGA 60			
QY	233	GGAGCTGGCGCGTGGGAACGCTCTGTGTGTATGTCTGTGAGACGGGCTGATGACAGAGT 292			
DB	61	GGAGCTGGCGCGTGGGAACGCTCTGTGTGTATGTCTGTGAGACGGGCTGATGACAGAGT 120			
QY	293	GGTGAACGGGCTCATGAGCGGCTGACTGGAGACCGCATCCAGAACCCCTGTGTAG 352			
DB	121	GGTGAACGGGCTCATGAGCGGCTGACTGGAGACCGCATCCAGAACCCCTGTGTAG 180			
QY	353	CCTCCACGAGGCTCTGGCAACGCGCTGGCAGCTTCTTGAACCATTTATGCTGGCTATGA 412			
DB	181	CCTCCACGAGGCTCTGGCAACGCGCTGGCAGCTTCTTGAACCATTTATGCTGGCTATGA 240			
QY	413	GCAGGTCAACAATGAAGACCTCTGACCAACTGACAGCTATGTGTGCGCGGCTGCT 472			
DB	241	GCAGGTCAACAATGAAGACCTCTGACCAACTGACAGCTATGTGTGCGCGGCTGCT 300			
QY	473	GTCAACCATGAACCTGTCTGTCTGCAACGCGCTTGGGGCTGCGCCTCTTCTGTGTCT 532			
DB	301	GTCAACCATGAACCTGTCTGTCTGCAACGCGCTTGGGGCTGCGCCTCTTCTGTGTCT 360			
QY	533	CAGCCTGGCCTTGGGGCTTCAATGCTGATGTGGACCTA-GAGAGTGAAGATATCGGCGTC 591			
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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FEATURES
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235	7	1.8	513	9	US-09-833-745-49	Sequence 49, Appl	308	1.6	14	US-10-345-871-177	Sequence 177, App
236	7	1.8	526	16	US-10-437-963-141300	Sequence 141300,	309	1.6	14	US-10-445-871-178	Sequence 178, App
237	7	1.8	539	15	US-10-424-599-276981	Sequence 276981,	310	1.6	14	US-10-253-286-177	Sequence 177, App
238	7	1.8	554	14	US-10-156-761-11033	Sequence 11033, A	311	1.6	14	US-10-253-286-178	Sequence 178, App
239	7	1.8	557	16	US-10-437-963-125622	Sequence 125622,	312	1.6	18	US-10-336-312-4	Sequence 4, Appli
240	7	1.8	567	16	US-10-437-963-106841	Sequence 106841,	313	1.6	18	US-10-336-312-28	Sequence 28, Appli
241	7	1.8	574	15	US-10-369-493-2580	Sequence 2580, Ap	314	1.6	18	US-10-336-312-29	Sequence 29, Appl
242	7	1.8	583	16	US-10-437-963-186085	Sequence 186085,	315	1.6	19	US-09-864-761-39076	Sequence 39076, A
243	7	1.8	586	15	US-10-282-122A-44727	Sequence 44727, A	316	1.6	19	US-10-245-871-179	Sequence 179, App
244	7	1.8	590	14	US-10-156-761-13221	Sequence 13221, A	317	1.6	19	US-10-253-286-179	Sequence 256, App
245	7	1.8	602	15	US-10-369-493-3842	Sequence 3842, Ap	318	1.6	21	US-09-965-738-296	Sequence 296, App
246	7	1.8	605	14	US-10-017-161-1768	Sequence 1768, Ap	319	1.6	22	US-10-207-655-312	Sequence 312, App
247	7	1.8	605	15	US-10-292-798-1424	Sequence 1424, Ap	320	1.6	24	US-10-642-289-19	Sequence 19, Appl
248	7	1.8	617	9	US-09-817-676A-12	Sequence 12, Appl	321	1.6	25	US-10-483-810-12	Sequence 12, Appl
249	7	1.8	617	16	US-10-830-677-12	Sequence 12, Appl	322	1.6	26	US-09-864-761-43552	Sequence 43552, A
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251	7	1.8	618	10	US-09-791-254-8	Sequence 8, Appli	324	1.6	28	US-09-864-761-42702	Sequence 42702, A
252	7	1.8	618	10	US-09-791-254-9	Sequence 9, Appli	325	1.6	28	US-10-092-750-26	Sequence 26, Appl
253	7	1.8	618	10	US-09-791-254-10	Sequence 10, Appl	326	1.6	31	US-10-029-386-31564	Sequence 31564, A
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259	7	1.8	676	14	US-10-096-840D-4	Sequence 4, Appli	332	1.6	36	US-10-000-256A-237	Sequence 237, App
260	7	1.8	683	16	US-10-308-163-12	Sequence 12, Appl	333	1.6	36	US-10-253-471-1269	Sequence 1269, Ap
261	7	1.8	683	16	US-10-725-189-12	Sequence 12, Appl	334	1.6	36	US-10-453-493-1269	Sequence 1269, Ap
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267	7	1.8	826	16	US-10-437-963-194781	Sequence 8653, Ap	340	1.6	41	US-09-985-153-136	Sequence 136, App
268	7	1.8	882	17	US-10-732-923-8653	Sequence 8653, Ap	341	1.6	41	US-10-425-115-246381	Sequence 246381, A
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271	7	1.8	1035	17	US-10-433-757-6	Sequence 6, Appli	344	1.6	45	US-09-764-891-5164	Sequence 5164, Ap
272	7	1.8	1080	14	US-10-205-219-62	Sequence 62, Appl	345	1.6	45	US-10-424-599-154736	Sequence 154736, A
273	7	1.8	1116	15	US-10-263-929-123	Sequence 123, App	346	1.6	45	US-10-424-599-196976	Sequence 196976, A
274	7	1.8	1167	16	US-10-437-963-128414	Sequence 128414,	347	1.6	45	US-10-424-599-250339	Sequence 250339, A
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276	7	1.8	1212	14	US-10-128-714-8471	Sequence 8471, Ap	349	1.6	45	US-10-276-774-2564	Sequence 2564, Ap
277	7	1.8	1213	9	US-09-969-515-8	Sequence 8, Appli	350	1.6	45	US-10-767-701-32633	Sequence 32633, A
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280	7	1.8	1266	15	US-10-210-130-124	Sequence 124, App	353	1.6	47	US-10-283-940-34	Sequence 34, Appl
281	7	1.8	1268	15	US-10-276-774-2072	Sequence 2072, Ap	354	1.6	47	US-10-424-599-160174	Sequence 160174, A
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283	7	1.8	1333	16	US-10-408-765A-119	Sequence 119, App	356	1.6	47	US-10-767-701-60313	Sequence 60313, A
284	7	1.8	1333	16	US-10-408-765A-2371	Sequence 2371, Ap	357	1.6	48	US-10-425-115-259806	Sequence 259806, A
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294	7	1.8	9234	17	US-09-942-025-13	Sequence 13, Appl	367	1.6	50	US-10-642-289-41	Sequence 41, Appl
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297	6	1.6	9	15	US-10-253-286-174	Sequence 174, App	370	1.6	50	US-10-425-115-350597	Sequence 350597, A
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378	6	1.6	52	15	US-10-424-599-273872	Sequence 273872, App	451	6	1.6	59	16	US-10-764-324-1063	Sequence 1063, App
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380	6	1.6	52	16	US-10-425-115-272070	Sequence 272070, App	453	6	1.6	59	16	US-10-764-324-1074	Sequence 1074, App
381	6	1.6	53	10	US-09-764-891-3100	Sequence 3100, App	454	6	1.6	59	16	US-10-764-324-1465	Sequence 1465, App
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392	6	1.6	55	14	US-10-008-524A-147	Sequence 147, App	465	6	1.6	61	14	US-10-424-599-204668	Sequence 204668, App
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394	6	1.6	55	16	US-10-437-963-117371	Sequence 117371, App	467	6	1.6	61	15	US-10-424-599-282823	Sequence 282823, App
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403	6	1.6	56	16	US-10-424-599-255520	Sequence 255520, App	476	6	1.6	62	16	US-10-425-115-270106	Sequence 270106, App
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410	6	1.6	57	15	US-10-424-599-210124	Sequence 210124, App	483	6	1.6	64	14	US-10-156-761-9421	Sequence 9421, App
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418	6	1.6	58	15	US-10-424-599-198180	Sequence 198180, App	491	6	1.6	64	16	US-10-425-115-269977	Sequence 269977, App
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429	6	1.6	59	14	US-10-040-862-1063	Sequence 1063, App	502	6	1.6	66	15	US-10-424-599-280331	Sequence 280331, App
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433	6	1.6	59	14	US-10-040-862-1639	Sequence 1639, App	506	6	1.6	66	16	US-10-425-115-209514	Sequence 209514, App
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438	6	1.6	59	15	US-10-057-475B-1074	Sequence 1074, App	511	6	1.6	67	15	US-10-424-599-260417	Sequence 260417, App
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444	6	1.6	59	15	US-10-154-884B-1069	Sequence 1069, App	517	6	1.6	68	15	US-10-424-599-154779	Sequence 154779, App
445	6	1.6	59	15	US-10-154-884B-1074	Sequence 1074, App	518	6	1.6	68	15	US-10-424-599-183255	Sequence 183255, App
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ALIGNMENTS

RESULT 1
US-10-642-289-2
; Sequence 2, Application US/10642289
; Publication No. US20040132053A1
; GENERAL INFORMATION:
; APPLICANT: PITSON, Stuart M
; APPLICANT: Brian, WATTENBERG W
; APPLICANT: Pu, XIA
; APPLICANT: Richard, D'ANDREA J
; APPLICANT: Jennifer, BABLE R
; APPLICANT: Mathew, VADAS A
; TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
; FILE REFERENCE: PITSON=1
; CURRENT APPLICATION NUMBER: US/10/642,289
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/959,897
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/AU00/00457
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: AU PQ 0339
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: AU PQ 1504
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-642-289-2

Query Match 100.0%; Score 384; DB 16; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-970-516-2
; Sequence 2, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-516-2

Query Match 87.5%; Score 336; DB 9; Length 384;
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US-10-354-358-26			
; Sequence 26, Application US/10354358			
; Publication No. US20030157082A1			
; GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc			
; APPLICANT: MacBeth, Kyle J.			
; APPLICANT: Tsai, Fong-Ying			
; APPLICANT: Lesoon, Andrea			
; APPLICANT: Lightcap, Eric S.			
; APPLICANT: Williamson, Mark			
; APPLICANT: Rudolph-Owen, Laura A.			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING			
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,			
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,			
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,			
; TITLE OF INVENTION: 9389, 1649, 85269, 10297, 1584, 9525, 14124, 4469,			
; TITLE OF INVENTION: 8950, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,			
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,			
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES			
; FILE REFERENCE: MPI02-020P1RNNOMNI			
; CURRENT APPLICATION NUMBER: US/10/354,358			
; CURRENT FILING DATE: 2003-01-30			
; PRIOR APPLICATION NUMBER: US 60/353,600			
; PRIOR FILING DATE: 2002-01-31			
; PRIOR APPLICATION NUMBER: US 60/364,517			
; PRIOR FILING DATE: 2002-03-15			
; PRIOR APPLICATION NUMBER: US 60/371,075			
; PRIOR FILING DATE: 2002-04-09			
; PRIOR APPLICATION NUMBER: US 60/371,507			
; PRIOR FILING DATE: 2002-04-10			
; PRIOR APPLICATION NUMBER: US 60/372,984			
; PRIOR FILING DATE: 2002-04-16			
; PRIOR APPLICATION NUMBER: US 60/374,194			
; PRIOR FILING DATE: 2002-04-19			
; PRIOR APPLICATION NUMBER: US 60/382,995			
; PRIOR FILING DATE: 2002-05-24			
; PRIOR APPLICATION NUMBER: US 60/385,023			
; PRIOR FILING DATE: 2002-05-31			
; PRIOR APPLICATION NUMBER: US 60/388,853			
; PRIOR FILING DATE: 2002-06-14			
; PRIOR APPLICATION NUMBER: US 60/389,395			
; PRIOR FILING DATE: 2002-06-17			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 122			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 26			
; LENGTH: 384			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-354-358-26			
Query Match 87.5%; Score 336; DB 14; Length 384;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MDPAGGPRGVLPRPCRVLLNPRGGKALQFRSHVQPLLAFAEISFTLMLTERRNHA	60
Db	1	MDPAGGPRGVLPRPCRVLLNPRGGKALQFRSHVQPLLAFAEISFTLMLTERRNHA	60
Qy	61	RELVRSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL	120
Db	61	RELVRSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL	120
Qy	121	NYAGYEQVTNEDLLTNCITLLCRLLSPMNLSSHTASGLRFLSVLSLAWGFADVDLE	180
Db	121	NYAGYEQVTNEDLLTNCITLLCRLLSPMNLSSHTASGLRFLSVLSLAWGFADVDLE	180
Qy	181	SEKYRRLGEMRFTLTGTFLLAALRTYRGLAYLPVGRVSGKTPASPVVVQQGPVDAHLVP	240
Db	181	SEKYRRLGEMRFTLTGTFLLAALRTYRGLAYLPVGRVSGKTPASPVVVQQGPVDAHLVP	240
Qy	241	LEEPVPSHTVVPDEDFVLVLLSHLHSGEMFAAPMGRCAGVGMHLFVYRAGVSRAML	300
Db	241	LEEPVPSHTVVPDEDFVLVLLSHLHSGEMFAAPMGRCAGVGMHLFVYRAGVSRAML	300
Qy	301	RLFLAMEKGRHMEYECPYLVVVPVAFRLPKDGKG	336
Db	301	RLFLAMEKGRHMEYECPYLVVVPVAFRLPKDGKG	336
RESULT 5			
US-10-715-117-2			
; Sequence 2, Application US/10715117			

```
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANKIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-2

Query Match      86.7%; Score 333; DB 16; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.2e-316;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 AGGPRGVLP RCRVLVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHAREL 63
Db  18 AGGPRGVLP RCRVLVLLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHAREL 77
QY  64 VSEELGRWDALV VMSGDGLMHEV VNGLMERDWTETAI QKPLCSLPAGSGNALAASLNHY 123
Db  78 VSEELGRWDALV VMSGDGLMHEV VNGLMERDWTETAI QKPLCSLPAGSGNALAASLNHY 137
QY  124 AGYEQVTTNEDLLT NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEK 183
Db  138 AGYEQVTTNEDLLT NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEK 197
QY  184 YRRLGEMRFTLGT FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEE 243
Db  198 YRRLGEMRFTLGT FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEE 257
QY  244 PVPSSHWTVPD DFLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFL 303
Db  258 PVPSSHWTVPD DFLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFL 317
QY  304 LAMEKGRHMEYEC PYLVVVPVAFRL EPKDGK 336
Db  318 LAMEKGRHMEYEC PYLVVVPVAFRL EPKDGK 350

RESULT 6
US-10-053-510-21
; Sequence 21, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrest, Henrik
; TITLE OF INVENTION: SPRINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-510-21

Query Match      83.3%; Score 320; DB 14; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-303;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e-303;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  17 VLVLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHARELVRSEELGRWDALV 76
Db  1 VLVLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHARELVRSEELGRWDALV 60
QY  77 VMSGDGLMHEV VNGLMERPDWETAI QKPLCSLPAGSGNALAASLNHYAGYEQVTTNEDLLT 136
Db  61 VMSGDGLMHEV VNGLMERPDWETAI QKPLCSLPAGSGNALAASLNHYAGYEQVTTNEDLLT 120
QY  137 NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEKYRRLGEMRFTLGT 196
Db  121 NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEKYRRLGEMRFTLGT 180
QY  197 FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEEPVPSHWTVPD 256
Db  181 FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEEPVPSHWTVPD 240
QY  257 FVLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 316
Db  241 FVLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 300
QY  317 PYLVVVPVAFRL EPKDGK 336
Db  301 PYLVVVPVAFRL EPKDGK 320

RESULT 7
US-10-348-052-21
; Sequence 21, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrest, Henrik
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348,052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-052-21

Query Match      83.3%; Score 320; DB 15; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-303;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  17 VLVLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHARELVRSEELGRWDALV 76
Db  1 VLVLNPRGGKGKALQ LFRSHVQPLLA EAEISFTLMLTERRNHARELVRSEELGRWDALV 60
QY  77 VMSGDGLMHEV VNGLMERPDWETAI QKPLCSLPAGSGNALAASLNHYAGYEQVTTNEDLLT 136
Db  61 VMSGDGLMHEV VNGLMERPDWETAI QKPLCSLPAGSGNALAASLNHYAGYEQVTTNEDLLT 120
QY  137 NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEKYRRLGEMRFTLGT 196
Db  121 NCTLLCRLLSPMNL LSLHTASGLR LFSVLSLANGFIADVDLESEKYRRLGEMRFTLGT 180
QY  197 FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEEPVPSHWTVPD 256
Db  181 FLRLAALRTYRGLAY L PVRGVSKT PTPASPVVVOQGPVD AHLVPLEEPVPSHWTVPD 240
QY  257 FVLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 316
Db  241 FVLVLALLHSHLGSEMF AAPMGRCAAGVMHLFYVRAGVSRAMLRLFLAMEKGRHMEYEC 300
QY  317 PYLVVVPVAFRL EPKDGK 336
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; SEQ ID NO 1
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 354
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-479-933-1

Query Match      74.7%; Score 287; DB 17; Length 384;
Best Local Similarity 100.0%; Pred. No. 3.4e-271; Indels 0; Gaps 0;
Matches 287; Conservative 0; Mismatches 0;

QY 1 MDPAGGPRGVLPKCRVLVLNPRGGKGKALQLFRRSHVQPLLAEEAIEISFTLMLTERRNHA 60
DB 1 MDPAGGPRGVLPKCRVLVLNPRGGKGKALQLFRRSHVQPLLAEEAIEISFTLMLTERRNHA 60
QY 61 RELVRSSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
DB 61 RELVRSSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
QY 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSIANGFIADVDLE 180
DB 121 NHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSIANGFIADVDLE 180
QY 181 SEKYYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVVQQGPVDAHLVP 240
DB 181 SEKYYRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVVQQGPVDAHLVP 240
QY 241 LEEPVPSTWTVPPDDEFVLVLALLSHLSEMFAPMGRCAAGVMHL 287
DB 241 LEEPVPSTWTVPPDDEFVLVLALLSHLSEMFAPMGRCAAGVMHL 287

RESULT 10
US-10-264-237-2585
; Sequence 2585, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI31PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2585
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2585

Query Match      74.2%; Score 285; DB 15; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.7e-269; Indels 0; Gaps 0;
Matches 285; Conservative 0; Mismatches 0;

QY 52 MLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAG 111
DB 1 MLTERRNHARELVRSEELGRWDALVVMGSDGLMHEVNVNGLMERPDWETAIOKPLCSLPAG 60
QY 112 SGNALAASLNHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAW 171
DB 61 SGNALAASLNHYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFSVLSLAW 120
QY 172 GFIAVDVLESEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVQQ 231
DB 121 GFIAVDVLESEKYRRLGEMRFTLGTFLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVQQ 180
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; SEQ ID NO 301
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 354
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-622-011-21

Query Match      83.3%; Score 320; DB 16; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-303; Indels 0; Gaps 0;
Matches 320; Conservative 0; Mismatches 0;

QY 17 VLVLNPRGGKGKALQLFRRSHVQPLLAEEAIEISFTLMLTERRNHARELVRSEELGRWDALV 76
DB 1 VLVLNPRGGKGKALQLFRRSHVQPLLAEEAIEISFTLMLTERRNHARELVRSEELGRWDALV 60
QY 77 VMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
DB 61 VMSGDGLMHEVNVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 120
QY 137 NCTLLCRLLSPMNLISLHTASGLRFSVLSIANGFIADVDLESEKYRRLGEMRFTLGT 196
DB 121 NCTLLCRLLSPMNLISLHTASGLRFSVLSIANGFIADVDLESEKYRRLGEMRFTLGT 180
QY 197 FLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVVQQGPVDAHLVPLEPVPSTWTVPPDED 256
DB 181 FLRLAALRTYRGLAYLPVGRVSGSKTPASPVVVVQQGPVDAHLVPLEPVPSTWTVPPDED 240
QY 257 FVLVLALLSHLSEMFAPMGRCAAGVMHLFVVRAGVSRAMLLRFLAMEKGRHMEYEC 316
DB 241 FVLVLALLSHLSEMFAPMGRCAAGVMHLFVVRAGVSRAMLLRFLAMEKGRHMEYEC 300
QY 317 PYLVVVPVVAFLRLEPKDGKG 336
DB 301 PYLVVVPVVAFLRLEPKDGKG 320

RESULT 9
US-10-479-933-1
; Sequence 1, Application US/10479933
; Publication No. US20050100547A1
; GENERAL INFORMATION:
; APPLICANT: Xia, Pu
; APPLICANT: Wang, Lijun
; APPLICANT: Vadas, Mathew
; APPLICANT: Gamble, Jennifer
; APPLICANT: Moretti, Paul
; APPLICANT: Pitson, Stuart
; TITLE OF INVENTION: SPHINGOSINE KINASE INTERACTS WITH TRAF2 AND
; TITLE OF INVENTION: MODULATES TUMOR NECROSIS FACTOR-INDUCED CELLULAR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 650063.401USPC
; CURRENT APPLICATION NUMBER: US/10/479,933
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/AU02/00710
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
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QY 232 GPDVDAHLVPLEPVPVSHWTVVDEDFVLVLLHSHLGSEMAAPMGRCAAGVMHLFYVR 291
Db 181 GPDVDAHLVPLEPVPVSHWTVVDEDFVLVLLHSHLGSEMAAPMGRCAAGVMHLFYVR 240
QY 292 AGVSRAMLRLFLAMEKGRHMEYECPLYVYVPVAFRLPEPKDGKG 336
Db 241 AGVSRAMLRLFLAMEKGRHMEYECPLYVYVPVAFRLPEPKDGKG 285
RESULT 11
US-09-796-487-3
; Sequence 3, Application US/09796487
; Patent No. US20020042358A1
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
; FILE REFERENCE: 07320001aa (2033957-0001)
; CURRENT APPLICATION NUMBER: US/09/796,487
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,532
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/530,868
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(384)
; OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspond-
; ing to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of Ge-
; nbank accession number AAF73423.
; PUBLICATION INFORMATION:
; AUTHORS: Nava et al.
; TITLE: Functional characterization of human spingosine kinase-1
; JOURNAL: FEBS Lett.
; VOLUME: 473
; ISSUE: 1
; PAGES: 81-84
; DATE: 2000
; DATABASE ACCESSION NUMBER: AAF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAF73423
; DATABASE ENTRY DATE: 2000-06-01
; RELEVANT RESIDUES: (1)..(384)
US-09-796-487-3

Query Match 65.1%; Score 250; DB 9; Length 384;
Best Local Similarity 100.0%; Pred. No. 4.6e-235;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPAGGPRGVLPVPCRVLLNPRGGKGKALQLFPSHVQPLLAEEAIEISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPVPCRVLLNPRGGKGKALQLFPSHVQPLLAEEAIEISFTMLTERRNHA 60
QY 61 RELVRSSEELGRWDALVVMGSDGLMHEVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSEELGRWDALVVMGSDGLMHEVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
QY 121 NYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Db 121 NYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
QY 181 SEKYYRLGEMRFTLTGTFRLAALRYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240
Db 181 SEKYYRLGEMRFTLTGTFRLAALRYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240
QY 241 LEEPVPVSHWT 250
Db 241 LEEPVPVSHWT 250
US-09-796-487-3

Db 241 LEEPVPVSHWT 250
RESULT 12
US-10-723-860-722
; Sequence 722, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 722
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-722

Query Match 65.1%; Score 250; DB 16; Length 384;
Best Local Similarity 100.0%; Pred. No. 4.6e-235;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPAGGPRGVLPVPCRVLLNPRGGKGKALQLFPSHVQPLLAEEAIEISFTMLTERRNHA 60
Db 1 MDPAGGPRGVLPVPCRVLLNPRGGKGKALQLFPSHVQPLLAEEAIEISFTMLTERRNHA 60
QY 61 RELVRSSEELGRWDALVVMGSDGLMHEVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
Db 61 RELVRSSEELGRWDALVVMGSDGLMHEVVGMLMERPDWETAIOKPLCSLPAGSGNALAASL 120
QY 121 NYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
Db 121 NYAGYEQVTNEDLLTNCITLLCRLLSPMNLISLHTASGLRFLSVLSLAWGFIADVDLE 180
QY 181 SEKYYRLGEMRFTLTGTFRLAALRYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240
Db 181 SEKYYRLGEMRFTLTGTFRLAALRYRGLAYLPVGRVGSKTPTASPVVVOQGPVDHLVP 240
QY 241 LEEPVPVSHWT 250
Db 241 LEEPVPVSHWT 250

RESULT 13
US-09-933-767-328
; Sequence 328, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885

;
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18

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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1998-01-30
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; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 328
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-933-767-328

Query Match 54.4%; Score 209; DB 10; Length 293;
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Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 QVTNEDLLTNCCTLLCRRLLSPMNLSSLHTASGLRLFSVLSAWGFIADVLESEKYRRL 96

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QY 248 HMTVPDDEDFVLVLLHSHLGSEMPAAPMGRCAGVMHLFYVRAGVSRAMLRLFLAME 307
Db 157 HMTVPDDEDFVLVLLHSHLGSEMPAAPMGRCAGVMHLFYVRAGVSRAMLRLFLAME 216

QY 308 KGRHMEYECPLYVVPVVAFRLEPKDKGK 336
Db 217 KGRHMEYECPLYVVPVVAFRLEPKDKGK 245

RESULT 14
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; Sequence 328, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 328

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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-328

Query Match      54.4%; Score 209; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.9e-195;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 217 KGRHMEYECPLYVYPVVAFRLEPKDGK 245

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; Sequence 328, Application US/10023282
; Publication NO. US20030092893A1
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; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
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; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 328
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-023-282-328
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Best Local Similarity 100.0%; Pred. No. 3.9e-195;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 QVTNEDLLTNCITLLCRLLSPNNLLSLHTASGLRFLSVLSLAWGFIADVDLSEKYYRL 187
Db 37 QVTNEDLLTNCITLLCRLLSPNNLLSLHTASGLRFLSVLSLAWGFIADVDLSEKYYRL 96

QY 188 GEMRFTLGTFLRLAALRTYGRGLAYLPVGRVGSKTTPASPVVQQGPVD AHLVPLEEPVPS 247
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Job time : 175 secs

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